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<b>(54) Title:</b> NEW NUCLEOTIDE SEQUENCES  <b>(57) Abstract</b>  The present invention relates to a nucleic acid molecule encoding a GABA <sub>B</sub> receptor, or a functionally equivalent modified form thereof, said receptor being selected from the group consisting of human and canine GABA <sub>B</sub> receptors.		

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## NEW NUCLEOTIDE SEQUENCES

## TECHNICAL FIELD

- 5 The present invention relates in particular to nucleic acid molecules encoding GABA<sub>B</sub> receptors, and to methods for screening for compounds which are inhibitors of transient lower esophageal sphincter relaxations (TLESR), said methods comprising the use of a nucleic acid molecule encoding a GABA<sub>B</sub> receptor.

10

## BACKGROUND ART

*GABA<sub>B</sub> receptors*

- 15 GABA (4-aminobutanoic acid) is an endogenous neurotransmitter in the central and peripheral nervous systems. Receptors for GABA have traditionally been divided into GABA<sub>A</sub> and GABA<sub>B</sub> receptor subtypes. GABA<sub>B</sub> receptors (for a review see Kerr, D.I.B. and Ong, J. (1995) Pharmac. Ther. vol. 67, pp.187-246) belong to the superfamily of G-protein coupled receptors. GABA<sub>B</sub> receptor agonists are described as being of use in the
- 20 treatment of CNS disorders, such as muscle relaxation in spinal spasticity, cardiovascular disorders, asthma, gut motility disorders such as irritable bowel syndrome and as prokinetic and anti-tussive agents. GABA<sub>B</sub> receptor agonists have also been disclosed as useful in the treatment of emesis (WO 96/11680).
- 25 The cloning of the rat GABA<sub>B</sub> receptors GABA<sub>B</sub>R1a (SEQ ID NOS: 44 and 45) and GABA<sub>B</sub>R1b (SEQ ID NOS: 46 and 47) is disclosed by Kaupmann et al. (1997) Nature, vol. 386, 239-246. The mature rat GABA<sub>B</sub>R1b differed from GABA<sub>B</sub>R1a in that the N-terminal 147 residues were replaced by 18 different residues. It was presumed that the rat GABA<sub>B</sub>R1a and -b receptor variants are derived from the same gene by alternative
- 30 splicing.

The cloning of the human GABA<sub>B</sub> receptor GABA<sub>B</sub>R1b is disclosed in WO 97/46675.

### *Reflux*

- 5 In some humans, the lower esophageal sphincter (LES) is prone to relaxing more frequently than in other humans. As a consequence, fluid from the stomach can pass into the esophagus since the mechanical barrier is temporarily lost at such times, an event hereinafter referred to as "reflux".
- 10 Gastro-esophageal reflux disease (GERD) is the most prevalent upper gastrointestinal tract disease. Current therapy has aimed at reducing gastric acid secretion, or by reducing esophageal acid exposure by enhancing esophageal clearance, lower esophageal sphincter tone and gastric emptying. The major mechanism behind reflux has been considered to depend on a hypotonic lower esophageal sphincter. However, recent research (e.g.
- 15 Holloway & Dent (1990) Gastroenterol. Clin. N. Amer. 19, 517-535) has shown that most reflux episodes occur during transient lower esophageal sphincter relaxations (TLESR), i.e. relaxations not triggered by swallows. It has also been shown that gastric acid secretion usually is normal in patients with GERD. Consequently, there is a need for compounds which reduce the incidence of TLESR and thereby prevent reflux.
- 20

### DISCLOSURE OF THE INVENTION

- In the applicants' earlier patent application WO 98/11885, filed on 15 September 1997, it is
- 25 disclosed that GABA<sub>B</sub> receptor agonists can be used to reduce the incidence of transient lower esophageal sphincter relaxations (TLESR).

- The present invention provides nucleic acid molecules encoding human and canine GABA<sub>B</sub> receptors. These nucleic acid molecules will make possible the screening for
- 30 compounds which are agonists or antagonists of GABA<sub>B</sub> receptors, e.g. compounds which are inhibitors of transient lower esophageal sphincter relaxations (TLESR).

Consequently, in a first aspect, the present invention provides a nucleic acid molecule encoding a GABA<sub>B</sub> receptor, or a functionally equivalent modified form thereof, said receptor being selected from the group consisting of human and canine GABA<sub>B</sub> receptors.

5 In preferred forms of the invention, the said nucleic acid molecule encodes the human GABA<sub>B</sub> receptor 1a (SEQ ID NOS: 48 and 49), 1b (SEQ ID NOS: 50 and 51), 1c (SEQ ID NOS: 54 and 55) or 1d (SEQ ID NOS: 56 and 57); or the canine GABA<sub>B</sub> receptor 1a (SEQ ID NOS: 52 and 53) or 1c (SEQ ID NOS: 58 and 59). Accordingly, the invention furthermore provides a nucleic acid molecule selected from:

- 10 (a) nucleic acid molecules comprising a nucleotide sequence set forth as SEQ ID NO: 48, 50, 52, 54, 56 or 58;
- (b) nucleic acid molecules comprising a nucleotide sequence capable of hybridizing, under stringent hybridization conditions, to a nucleotide sequence complementary to the polypeptide coding region of a DNA molecule as defined in (a); and
- 15 (c) nucleic acid molecules comprising a nucleotide sequence which is degenerate as a result of the genetic code to a nucleotide sequence as defined in (a) or (b).

Furthermore, the invention provides nucleic acid molecules of genomic origin encoding human GABA<sub>B</sub> receptors (SEQ ID NOS: 60 and 61) as well as nucleic acid molecules (set  
20 forth as SEQ ID NO: 70, 72, 74, 76, 78, 80, 82, 84) encoding additional isoforms of the human GABA<sub>B</sub> receptor which isoforms can be shown to be generated by alternative splicing.

It should thus be understood that the nucleic acid molecule according to the invention is  
25 not to be limited strictly to molecules comprising the sequences set forth as SEQ ID : 48, 50, 52, 54, 56 or 58. Rather the invention encompasses nucleic acid molecules carrying modifications like substitutions, small deletions, insertions or inversions, which nevertheless encode proteins having substantially the biochemical activity of the GABA<sub>B</sub> receptors according to the invention. Included in the invention are consequently nucleic  
30 acid molecules, the nucleotide sequence of which is at least 95% homologous, preferably at least 96%, 97%, 98% or 99% homologous, with the nucleotide sequence shown as SEQ ID NO: 48, 50, 52, 54, 56 or 58 in the Sequence Listing.

The term "stringent hybridization conditions" is known in the art from standard protocols (e.g. Current Protocols in Molecular Biology, editors F. Ausubel et al., John Wiley and Sons, Inc. 1994) and could be understood as as stringent or more stringent than those  
5 defined by e.g. hybridization to filter-bound DNA in 0.5 M NaHPO<sub>4</sub>, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at +65°C, and washing in 0.1xSSC / 0.1% SDS at +68°C.

Included in the invention is also a nucleic acid molecule which nucleotide sequence is degenerate, because of the genetic code, to a nucleic acid of the present invention and more  
10 particularly to one of the nucleotide sequences set forth as SEQ ID NOs: 48, 50, 52, 54, 56 and 58. A sequential grouping of three nucleotides, a "codon", codes for one amino acid. Since there are 64 possible codons, but only 20 natural amino acids, most amino acids are coded for by more than one codon. This natural "degeneracy", or "redundancy", of the genetic code is well known in the art. It will thus be appreciated that the nucleic acid  
15 sequences shown in the Sequence Listing is only an example within a large but definite group of nucleic acid sequences which will encode the polypeptide as described above.

In a further aspect, the invention provides a recombinant polypeptide encoded by a nucleotide sequence of the present invention, encoding a GABA<sub>B</sub> receptor. In preferred  
20 forms of the inventions, the said polypeptide comprises an amino acid sequence set forth as SEQ ID NO: 49, 51, 53, 55, 57, 59, 71, 73, 75, 77, 79, 81, 83 or 85 in the Sequence Listing. However, polypeptides of the present invention are not to limited to those having an amino acid sequence identical with one of SEQ ID NOs: 49, 51, 53, 55, 59, 71, 73, 75, 77, 79, 81, 83 or 85 in the Sequence Listing. Rather the invention encompasses polypeptides carrying  
25 modifications such as substitutions, small deletions, insertions or inversions, which polypeptides nevertheless have substantially the biological activities of the GABA<sub>B</sub> receptor. Included in the invention are consequently polypeptides, the amino acid sequence of which is at least 95% homologous, preferably at least 96%, 97%, 98% or 99% homologous, with one of the amino acid sequences described by SEQ ID NOs: 49, 51, 53,  
30 55, 57 59, 71, 73, 75, 77, 79, 81, 83 and 85 in the Sequence Listing.

Included in the invention are polypeptides of the present invention which have been post-translationally modified, e.g. by cleavage of an N-terminal signal sequence which can be e.g. 1 to 25 amino acids long.

- 5 In yet another aspect, the invention provides a vector transformed with a nucleic acid molecule of the present invention. The said vector can e.g. be a replicable expression vector which carries and is capable of mediating the expression of a nucleic acid molecule according to the invention. In the present context the term "replicable" means that the vector is able to replicate in a given type of host cell into which it has been introduced.
- 10 Examples of vectors are viruses such as bacteriophages, cosmids, plasmids and other recombination vectors. Nucleic acid molecules are inserted into vector genomes by methods well known in the art.

- Included in the invention is also a cultured host cell harbouring a vector according to the invention. Such a host cell can be a prokaryotic cell, a unicellular eukaryotic cell or a cell derived from a multicellular organism. The host cell can thus e.g. be a bacterial cell such as an *E. coli* cell; a cell from a yeast such as *Saccharomyces cerevisiae* or *Pichia pastoris*, or a mammalian cell. The methods employed to effect introduction of the vector into the host cell are standard methods well-known to a person familiar with recombinant DNA
- 15 methods.
- 20

- A further aspect of the invention is a process for production of a GABA<sub>B</sub> receptor polypeptide according to the invention, said process comprising culturing a host cell as defined above under conditions whereby the said polypeptide is produced, and recovering
- 25 the said polypeptide.

- A further important aspect of the invention is a method for the screening of compounds which are inhibitors of transient lower esophageal sphincter relaxations (TLESR), said method comprising the use of a nucleic acid molecule encoding a GABA<sub>B</sub> receptor. The
- 30 said nucleic acid molecule encoding a GABA<sub>B</sub> receptor can e.g. be one of the nucleic acid molecules according to the invention encoding human or canine GABA<sub>B</sub> receptors.
- However, it should be understood that this aspect of the invention is not limited to the use



of the said human and canine GABA<sub>B</sub> receptors, but rather encompasses the use of any GABA<sub>B</sub> receptor for screening for compounds which are inhibitors of transient lower esophageal sphincter relaxations.

- 5 In yet another important aspect, the invention provides a method for the screening of compounds which are agonists or antagonists to a GABA<sub>B</sub> receptor, said method comprising the use of a nucleic acid molecule, according to the invention, encoding human or canine GABA<sub>B</sub> receptors.

## 10 Brief Description of the Drawings

Figure 1: Map of the human GABA<sub>B</sub> receptor gene.

The exon/intron organisation is shown. Exons are indicated as solid boxes numbered 1-23.

- 15 The part of intron 5 that is retained together with exon 6 giving rise to GABA<sub>B</sub> receptor 1b is indicated as an open box.

Figure 2: Expression of human GABA<sub>B</sub> receptor 1b isoform in transfected C127 cells.

20

Western blot analysis of transfected C127 cells using a polyclonal anti-human GABA<sub>B</sub> receptor antibody. Lane 1: Untransfected C127 whole cell lysate. Lanes 2-7: Whole cell lysates of six independent clones transfected with human GABA<sub>B</sub> receptor 1b isoform encoding cDNA. The clones analysed in lanes 4 to 7 express a GABA<sub>B</sub> receptor of

25 expected molecular weight (arrow).

Figure 3: Expression of human GABA<sub>B</sub> receptor 1d isoform in transfected C127 cells.

- 30 Western blot analysis of transfected C127 cells using a polyclonal anti-human GABA<sub>B</sub> receptor antibody. Lanes 1-3: Concentrated culture media from three independent C127 clones transfected with a cDNA expression construct encoding the human GABA<sub>B</sub> receptor

1d isoform. Lanes 4-6: Whole cell lysates corresponding to the clones analysed in lanes 1-3. The experiment revealed that the human GABA<sub>B</sub> receptor 1d cDNA encodes a secreted isoform. The arrow indicates the bands corresponding to the 1d isoform.

5

Figure 4: Expression of human GABA<sub>B</sub> receptor 1d isoform in *E. coli*.

Western blot analysis of transformed *E. coli* cells using a polyclonal anti-human GABA<sub>B</sub> receptor antibody. Lane 1: Lysate from an uninduced *E. coli* culture transformed with an  
10 pET-based expression construct encoding the human GABA<sub>B</sub> receptor 1d cDNA. Lane 2:  
Lysate from an IPTG-induced *E. coli* culture transformed with an expression construct  
encoding the human GABA<sub>B</sub> receptor 1d cDNA. Lane 3: Lysate from an IPTG-induced  
*E. coli* culture transformed with an expression construct encoding an unrelated protein.  
Lane 4: The BSA-conjugated peptide previously used for immunization was loaded on the  
15 gel as a positive antibody control.

The screening methods according to the invention can e.g. comprise the steps (a)  
transforming a cultured cell with a nucleic acid molecule encoding a GABA<sub>B</sub> receptor, so  
20 that a GABA<sub>B</sub> receptor is expressed on the surface of the cell; (b) contacting a test  
compound with the said cell; and (c) determining whether the test compound binds to,  
and/or activates, the GABA<sub>B</sub> receptor.

In particular GABA<sub>B</sub> receptor expressing cells, transgenic animals or cells and tissues  
25 derived thereof, may be used to screen substance libraries for antagonist or agonist  
activities. For this purpose, GABA<sub>B</sub> receptor expression may be directed to cells and  
tissues containing, either naturally or artificially, the necessary components allowing  
correct receptor transport and processing as well as coupling to second messenger  
pathways. Screening may be performed as ligand binding assays or functional assays. For  
30 screening, cells and tissues may be prepared in various ways, each uniquely suited to its  
purpose. Ligand binding assays are performed *in vivo* or *in vitro* using e.g. radiolabelled  
GABA. Functional assays exemplified by, but not limited to, Ca<sup>++</sup>-responses, cAMP-

responses and effects on  $K^+$  channels, may be performed in living cells, broken cells, isolated cell membranes, as well as in tissues and in living animals. To facilitate measurement of physiological GABA<sub>B</sub> receptor mediated responses, GABA<sub>B</sub> receptors may be co-expressed with promiscuous G-proteins like e.g. G $\alpha$ 16 or Gq15 increasing G-protein coupling. Another possible way to increase G-protein coupling is to fuse the GABA<sub>B</sub> receptor with appropriate G-proteins using standard molecular techniques. In order to further improve readouts in  $Ca^{++}$ -response assays, GABA<sub>B</sub> receptors may be co-expressed with aequorin, a photoprotein cloned from the luminescent jellyfish *Aequorea victoria*.

10

In yet another aspect, the invention provides a pharmaceutical compositions comprising a soluble GABA<sub>B</sub> receptor further comprising one or more pharmaceutical acceptable carriers and/or diluents.

15 In yet another aspect, the invention provides a method for the diagnosis or treatment of conditions related to GABA-dysfunction, e.g. epilepsy, psychiatric disorders such as depression and anxiety, cognitive dysfunction, gastroesophageal reflux disease, emesis, irritable bowel syndrome, dyspepsia, spasticity, arthritis, allergies, autoimmune diseases, neoplastic diseases, pain, and infectious diseases, comprising the use or administration of soluble forms of the GABA<sub>B</sub> receptor, such as the human GABA<sub>B</sub> receptor 1c or 1d or functionally equivalent modified forms thereof; preferably being a polypeptide of the present invention..

20

The soluble forms of the GABA<sub>B</sub> receptor can e.g. be produced by culturing a host cell harbouring a vector comprising a nucleic acid encoding the soluble GABA<sub>B</sub> receptor under conditions where whereby the said polypeptide is produced, the polypeptide recovered and administered to a patient in need thereof.

25

30 Furthermore, the level of soluble GABA<sub>B</sub> receptors in certain body fluids, e.g. serum and CSF, can be measured and used in diagnostics related to conditions with altered levels of soluble GABA<sub>B</sub> receptors in said body fluids.

Throughout this description the terms "standard protocols" and "standard procedures", when used in the context of molecular cloning techniques, are to be understood as protocols and procedures found in an ordinary laboratory manual such as: Current Protocols in Molecular Biology, editors F. Ausubel et al., John Wiley and Sons, Inc. 1994, or Sambrook, J., Fritsch, E.F. and Maniatis, T., Molecular Cloning: A laboratory manual, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY 1989.

#### EXAMPLES

10

EXAMPLE 1A: Cloning and sequencing of cDNA encoding human GABA<sub>B</sub> receptor 1a and 1b

Messenger RNA from human hippocampus was obtained from Clontech (Palo Alto, CA, USA) (catalog #6578-1). First-strand cDNA synthesis reactions were performed using the First-strand cDNA Synthesis kit from Amersham Pharmacia Biotech (Uppsala, Sweden). The pd(N)<sub>6</sub> primer was used to prime the first-strand synthesis. The generated cDNA molecules were used as template in the PCR reactions described below.

20 Specific PCR primers were designed (Table 1) based on the sequences of the rat GABA<sub>B</sub> receptor 1a and 1b cDNA (Kaupmann et al. 1997, EMBL accession numbers Y10369 (SEQ ID NO: 44) and Y10370 (SEQ ID NO: 46)).

TABLE 1

Primers used for RT-PCR on mRNA from human hippocampus

Nr.	Species	Sequence 5' - 3'	SEQ ID NO
794	Rat	GTTTCTTCTCGGATCCAGCTGTGCCTG	1
795	Rat	CAGGCACAGCTGGATCCGAGAAGAACT	2
796	Rat	CGGTCGACTCACTTGTAAGCAAATGTACTCGACTCCC	3
797	Rat	ATGCGCGCCGGCAGCCAACATGCTGCTGCTGCTGCTGGTGC	4
831	Rat	CGGTCGACTCACTTGTAAGCAAATGTACTCGACTCCCATCACAGC	5
838	Rat	ATGCGCGCCGGCAGCCAACATGCTGCTGCTGCTGCTGGTGCCTCTCTCC	6
842	Rat	CAGGCACAGCTGGATCCGAGAAGAACTCTGTGCGAAAGT	7
863	Rat	GGTCATCCAGCGTTGAGGTGAAGAC	8
864	Rat	GAAGGTTGCCAGATTATACATCCGC	9
865	Rat	CCACGATGATTCGAGCATCTTGACG	10
866	Rat	GCCTCTCACTCCCCTCATCTCC	11
932	Human	GAGTGAAGGAGGCTGGAATTG	12

- 5 cDNA fragments encoding parts of the human GABA<sub>B</sub> receptors were amplified directly by PCR using the designed primers with the generated cDNA molecules as templates. All PCR experiments were carried out using the Perkin Elmer Taq DNA polymerase with Gene Amp (Roche Molecular Systems Inc., NJ, USA) with the following PCR program: +95°C for 1 minute, +50°C for 30 seconds, +72°C for 3 minutes, repeated 44 times and finally
- 10 +72°C for 7 minutes. The following primer combinations gave PCR products with expected sizes: 838 and 842, 838 and 795, 797 and 865, 864 and 865, 864 and 863 which corresponds to the 5'-end of the GABA<sub>B</sub> receptor 1a. Primer pair 932 and 831, 932 and 796, 794 and 831 gave PCR products which correspond to the 3'-end of both GABA<sub>B</sub> receptor 1a and 1b. The primer combination 839 and 918 gave a PCR product
- 15 corresponding to the 5'-end of the GABA<sub>B</sub> receptor 1b.

The PCR products were subcloned into the pGEM-T vector from Promega (Madison, USA). The inserts were subjected to nucleotide sequence analysis, the complete nucleotide sequence for all subclones were determined using a Thermo Sequenase dye terminator

20 cycle sequencing pre-mix kit (Amersham Pharmacia Biotech, Uppsala, Sweden). As primers for sequencing reactions specific oligonucleotides complementary to the vector pGEM-T or primers complementary to the cDNA encoding the GABA<sub>B</sub> receptor were used.

Additional PCR primers were designed based on the obtained sequences encoding fragments of the human GABA<sub>B</sub> receptor and additional DNA fragments encoding parts of the human GABA<sub>B</sub> receptors were amplified by PCR, the PCR products subcloned and  
5 sequenced as described above.

**EXAMPLE 1B : Cloning and sequencing of the 3'-ends of the cDNA encoding human GABA<sub>B</sub> receptors 1a and 1b**

Messenger RNA from human hippocampus was obtained from Clontech (Palo Alto, CA, USA) (catalogue #6578-1). First strand cDNA synthesis reactions were performed using the First-strand cDNA Synthesis kit from Amersham Pharmacia Biotech (Uppsala, Sweden). The Not I-d(T)<sub>18</sub> primer was used to prime the first-strand synthesis. The  
15 generated cDNA molecules were used as template in the PCR reactions described below.

Specific PCR primers were designed (Table 2 ) based on the sequences of the human GABA<sub>B</sub> receptor 1a and 1b cDNA obtained in Example 1A and the EST sequence EMBL accession number Y11044.

By homology searches in the EMBL database using the GABA<sub>B</sub> receptor cDNA sequences obtained in Example 1A as query the EST sequence EMBL accession number Y11044 have been found to be homologous to the 3'-end of the GABA<sub>B</sub> receptor cDNA.

**TABLE 2**

Primers used in PCR to amplify 3'ends of human GABA<sub>B</sub> receptor cDNA

Nr	Species	Sequence 5'-3'	SEQ ID NO
938	Human	GACGCTTATCGAGCAGCTTC	13
972	Human	AGCCCAGAACTCACAGGGGGACAT	14
973	Human	GCTTCAAGCCAGGTACGAATAA	15

cDNA fragments encoding parts of the human GABA<sub>B</sub> receptors were amplified directly by  
30 PCR using the designed primers with the generated cDNA molecules as templates. All

PCR experiments were carried out using the Perkin Elmer Taq DNA polymerase with Gene Amp (Roche Molecular Systems Inc., NJ, USA) with the following PCR program: + 95°C for 1 minute, +50°C for 30 seconds, +72°C for 3 minutes, repeated 44 times and finally +72°C for 7 minutes. The following primer combinations gave PCR products with expected sizes: 938 and 972, 938 and 973 corresponding to the 3' end of both GABA<sub>B</sub> receptor 1a and 1b cDNA.

The PCR products were subcloned into the pGEM-T vector from Promega (Madison, USA). The inserts were subjected to nucleotide sequence analysis, the complete nucleotide sequence for all subclones were determined using a Thermo Sequenase dye terminator cycle sequencing pre-mix kit (Amersham Pharmacia Biotech, Uppsala, Sweden). As primers for sequencing reactions specific oligonucleotides complementary to the vector pGEM-T or primers complementary to the cDNA encoding the GABA<sub>B</sub> receptor were used.

15

**EXAMPLE 1C : Cloning and sequencing of the 5'-end of the cDNA encoding human GABA<sub>B</sub> receptor 1b**

Messenger RNA from human hippocampus was obtained from Clontech (Palo Alto, CA, USA) (catalogue #6578-1). Marathon cDNA amplification Kit (Clontech) was used for performing 5'/3'- RACE (Rapid Amplification of cDNA Ends). Adaptor-ligated double stranded cDNA molecules were amplified according to the manufacturer's description. The pd(N)<sub>6</sub> primer from the First-strand cDNA Synthesis kit from Amersham Pharmacia Biotech (Uppsala, Sweden) was used to produce the adaptor-ligated cDNA.

25

A specific PCR primer was designed (Table 3) based on the sequences of the human GABA<sub>B</sub> receptor 1b cDNA obtained in Example 1A.

TABLE 3

Primers used in PCR to amplify the 5'-ends of human GABA<sub>B</sub> receptor cDNA

Nr.	Species	Sequence 5'-3'	SEQ ID NO
958	Human	TGGCCCTCCACCGCCTCAGTCATCTCA	16
AP1	Marathon kit	CCATCCTAATACGACTCACTATAGGGC	17

5 cDNA fragments encoding part of the human GABA<sub>B</sub> receptors were amplified directly by PCR using the designed primers with the generated adaptor-ligated cDNA molecules as template. The PCR experiment was carried out using the Expand Long Template PCR System (Boehringer Mannheim GmbH, Germany) with the following PCR program: + 94°C for 1minute, + 94°C for 30 seconds, +60°C for 30 seconds, +68°C for 4 minutes, 10 repeated 24 times. The primer combination AP1 and 958 gave a PCR product which corresponded to the 5'-end of the GABA<sub>B</sub> receptor 1b cDNA, including 190 base pairs upstream the initiation codon.

The PCR products were subcloned into the pGEM-T vector from Promega (Madison, 15 USA). The inserts were subjected to nucleotide sequence analysis, the complete nucleotide sequence for all subclones were determined using a Thermo Sequenase dye terminator cycle sequencing pre-mix kit (Amersham Pharmacia Biotech, Uppsala, Sweden). As primers for sequencing reactions specific oligonucleotides complementary to the vector pGEM-T or primers complementary to the cDNA encoding the GABA<sub>B</sub> receptor were 20 used.

EXAMPLE 1D : Cloning and sequencing of the 5'-end of the cDNA encoding human GABA<sub>B</sub> receptor 1a

25 Messenger RNA from human hippocampus was obtained from Clontech (Palo Alto, USA) (catalogue #6578-1). Marathon cDNA amplification Kit (Clontech) was used to obtain adaptor-ligated double stranded cDNA molecules according to the manufacturer's description. The pd(N)<sub>6</sub> primer from the First-strand cDNA Synthesis kit from Amersham 30 Pharmacia Biotech (Uppsala, Sweden) was used to obtain the adaptor-ligated cDNA .



Specific PCR primers were designed (Table 4) based on the sequences of the human GABA<sub>B</sub> receptor 1a cDNA obtained in Example 1 and the rat GABA<sub>B</sub> receptor 1a cDNA disclosed in WO 97/46675.

5

TABLE 4

Primers used to amplify 5'-ends of the human GABAB receptor 1a cDNA

Nr.	Species	Sequence 5'-3'	SEQ ID NO
1033	Human	CTCAATCTCATAGTCCACTGG	18
1087	Rat	CCTTGAGGCCCGGGGAGAG	19

- 10 cDNA fragments encoding part of the human GABAB 1a receptor were amplified directly by PCR using the designed primers with the generated adaptor-ligated cDNA molecules as template. The PCR was performed using the Perkin Elmer Taq DNA polymerase with Gene Amp (Roche Molecular Systems Inc., NJ, USA) with the following PCR program: +94°C for 1 minute, +50°C for 30 seconds, +72°C for 3 minutes; +94°C for 1 minute, +60°C  
15 for 30 seconds, +72°C for 4 minutes, repeated 34 times and finally +72°C for 7 minutes.

The primer combination 1087 and 1033 gave a PCR product corresponding to the 5'-end of the GABA<sub>B</sub> receptor 1a cDNA, including 26 base pairs upstream the initiation codon.

- 20 The PCR products were subcloned into the pGEM-T vector from Promega (Madison, USA). The inserts were subjected to nucleotide sequence analysis, the complete nucleotide sequence for all subclones were determined using a Thermo Sequenase dye terminator cycle sequencing pre-mix kit (Amersham Pharmacia Biotech, Uppsala, Sweden). As primers for sequencing reactions specific oligonucleotides complementary to the vector  
25 pGEM-T were used.

- A complete cDNA sequence encoding the human GABA<sub>B</sub> receptors 1a (SEQ ID NO: 48) and the human GABA<sub>B</sub> receptor 1b (SEQ ID NO: 50) were obtained by aligning the sequences of the different fragments cloned and sequenced in Examples 1A, 1B, 1C and  
30 1D.

# EXAMPLE 2A: Cloning and sequencing of cDNA encoding canine GABA<sub>B</sub> receptor 1a

- 5 QuickPrep Micro mRNA Purification kit (Amersham Pharmacia Biotech, Uppsala, Sweden) was used to isolate mRNA from canine neural tissues according to the manufacturers description. First-strand cDNA synthesis reactions were performed using the First-strand cDNA Synthesis kit from Amersham Pharmacia Biotech (Uppsala, Sweden). The Not-I-d(T)<sub>18</sub> bifunctional or pd(N)<sub>6</sub> primer was used to prime the first-strand synthesis.
- 10 The generated cDNA molecules were used as template in the PCR reactions described below.

Specific PCR primers (Table 5) were designed based on the sequences of the rat GABA<sub>B</sub> receptor 1a and 1b cDNA (Kaupmann et al. 1997, EMBL accession numbers Y10369 (SEQ ID NO: 44 and Y10370 (SEQ ID NO: 46)).

15

TABLE 5

Primers used for RT-PCR on mRNA from canine cortex

Nr.	Species	Sequence 5'-3'	SEQ ID NO
795	Rat	CAGGCACAGCTGGATCCGAGAAGAACT	20
831	Rat	CGGTCGACTCACTTGTAAGCAAATGTACTCGACTCCCATCACAGC	21
838	Rat	ATGCGCGCCGGCAGCCAACATGCTGCTGCTGCTGGTGCCTCTCTTCC	22
840	Rat	CGTCAAGATGCTCGAATCATCG	23
841	Rat	CAGGGGGCTCAGAGGGTCCC	24
842	Rat	CAGGCACAGCTGGATCCGAGAAGAACTCTGTGGAAAGT	25
844	Rat	CGGTCGACTCACTTGTAAGCAAATGTACTCGACTCCCATCACAGCTAAG	26
848	Rat	ACTTCCGACAGAGTTTCTTCTCGGATCCAGCTGTGCCTG	27
865	Rat	CCACGATGATTCGAGCATCTTGACG	28

20

cDNA fragments encoding parts of the canine GABA<sub>B</sub> receptor were amplified directly by PCR using the designed primers with the generated cDNA molecules as templates. All PCR experiments were carried out using the Perkin Elmer Taq DNA polymerase with Gene Amp (Roche Molecular Systems Inc., NJ, USA) with the following PCR program: +95°C for 1 minute, +50°C for 30 seconds, +72°C for 3 minutes, repeated 44 times and finally

25

+72°C for 7 minutes. The following primer combinations gave PCR products with expected sizes: 842 and 838, 838 and 795, 838 and 865 which corresponds to the 5'-part of the canine GABA<sub>B</sub> receptor cDNA. Primer pair 848 and 844, 848 and 831, 848 and 841, 840 and 841 gave PCR products which correspond to the 3'-part of the canine GABA<sub>B</sub> receptor cDNA.

The PCR products were subcloned into the pGEM-T vector from Promega (Madison, USA). The inserts were subjected to nucleotide sequence analysis, the complete nucleotide sequence for all subclones were determined using a Thermo Sequenase dye terminator cycle sequencing pre-mix kit (Amersham Pharmacia Biotech, Uppsala, Sweden). As primers for sequencing reactions specific oligonucleotides complementary to the vector pGEM-T or primers complementary to the cDNA encoding the GABA<sub>B</sub> receptor were used.

EXAMPLE 2B: Cloning and sequencing of the 3'- and 5'-ends of the cDNA encoding canine GABA<sub>B</sub> receptor 1a

QuickPrep Micro mRNA Purification kit (Amersham Pharmacia Biotech, Uppsala, Sweden) was used to isolate mRNA from canine nerve tissues according to the manufactures description. Marathon cDNA amplification Kit (Clontech, Palo Alto, CA, USA) were used for performing both 5'-and 3'-RACE. Two adaptor-ligated double stranded cDNA libraries were amplified according to the manufacturers description. A random primer (pd(N)<sub>6</sub>) was used when amplifying the adaptor-ligated cDNA for the 5'-RACE and the Marathon cDNA Synthesis primer (52-mer) was used when amplifying the adaptor ligated cDNA for the 3'-RACE.

Specific PCR primers were designed (Table 6) based on the sequence of canine GABA<sub>B</sub> receptor 1a cDNA obtained in Example 2A.

TABLE 6

Primers used in PCR to amplify the 5'- and 3'-ends of canine GABA<sub>B</sub> receptor 1a cDNA

Nr.	Species	Sequence 5'-3'	SEQ ID NO
936	canine	CTACCGCGCAATGAACTCCTCGTC	29
1076	canine	CGAGGTGGCGTTGGGGGTCTGTGC	30
AP1	Marathon kit	CCATCCTAATACGACTCACTATAGGGC	31
AP2	Marathon kit	ACTCACTATAGGGCTCGAGCGGC	32

5 cDNA fragments encoding parts of the canine GABA<sub>B</sub> receptor were amplified by PCR from the adaptor-ligated cDNA using the designed primers. A number of different PCR programs were tested to find conditions where PCR products corresponding to GABA<sub>B</sub> receptor DNA were obtained. The 5'- PCR experiments were carried out using the Expand Long Template PCR System (Boehringer Mannheim GmbH, Germany) with the following  
10 PCR program: +94°C for 30 seconds, +72°C for 3 minutes, repeated 4 times; +94°C for 30 seconds, +70°C for 3 minutes, repeated 4 times; and +94°C for 30 seconds, +68°C for 3 minutes, repeated 24 times. The primer combination AP2 and 1076 gave a PCR product which corresponded to the 5'-end of the GABA<sub>B</sub> receptor cDNA, including 114 base pairs upstream the initiation codon.

15

The 3'- PCR experiments were carried out using the Expand Long Template PCR System (Boehringer Mannheim GmbH, Germany) with the following PCR program: +94°C for 1 minute; and +94°C for 30 seconds, +60°C for 30 seconds, +68 °C for 4 minutes, repeated 29 times. The primer combination AP1 and 936 gave a PCR fragment which corresponded  
20 to the 3'-end of the GABA<sub>B</sub> receptor cDNA, including the poly(A) tail.

The PCR products were subcloned into the pGEM-T vector from Promega (Madison, USA). The inserts were subjected to nucleotide sequence analysis, the complete nucleotide sequence for all subclones were determined using a Thermo Sequenase dye terminator  
25 cycle sequencing pre-mix kit (Amersham Pharmacia Biotech, Uppsala, Sweden). As primers for sequencing reactions specific oligonucleotides complementary to the vector pGEM-T or primers complementary to GABA<sub>B</sub> receptor DNA were used.

Complete cDNA sequence encoding the canine GABA<sub>B</sub> receptor 1a (SEQ ID NO: 52) was obtained by aligning the sequences of the different fragments obtained in Example 2A and Example 2B.

5

EXAMPLE 3A: Cloning of cDNA encoding human GABA<sub>B</sub> receptor 1c and 1d from Jurkat cells

A guanidinisothiocyanate/CsCl method was used to isolate total RNA from Jurkat cells.

10 The first-strand cDNA synthesis was performed using the First-strand cDNA Synthesis kit from Amersham Pharmacia Biotech (Uppsala, Sweden). The pd(N)<sub>6</sub> primer was used to prime the first strand synthesis. The generated cDNA molecules were used as templates in the PCR reaction described below.

15 Specific PCR primers (Table 7) were designed based on the sequence of human GABA<sub>B</sub> receptor 1a and 1b cDNA (Example 1), rat GABA<sub>B</sub> receptor (Kaupmann et al. 1997) and the EST sequence EMBL accession number Y11044.

TABLE 7

20 Primers used in RT-PCR on mRNA from Jurkat cells

Nr	Species	Sequence 5'-3'	SEQ ID NO
938	human	GACGCTTATCGAGCAGCTTC	33
972	human	AGCCCAGAACTCACAGGGGGACAT	34
973	human	GCTTCAAGCCAGGTACGAACTAA	35
893	rat	GGAGCACCCCAAGCCCCACTG	36
937	human	CTGGTTCCTCCCAATGTG	37
1005	rat	CCTCTACTCCCCTCATCTC	38
1030	human	AAGCCAACCTTCCTGCTTCTC	39

cDNA fragments encoding parts of the GABA<sub>B</sub> receptor were amplified directly by PCR using human and rat specific primers. All PCR experiments were carried out using the  
 25 Perkin Elmer Taq DNA polymerase with Gene Amp (Roche Molecular Systems Inc., NJ,

USA) with the following PCR program: +95°C for 1 minute; +54°C for 1 minutes, +72°C for 3 minutes, repeated 44 times; and finally +72°C for 7 minutes.

The PCR products were subcloned into the pGEM-T vector from Promega (Madison, USA). The inserts were subjected to nucleotide sequence analysis, the complete nucleotide sequence for all subclones were determined using a Thermo Sequenase dye terminator cycle sequencing pre-mix kit (Amersham Pharmacia Biotech, Uppsala, Sweden). As primers for sequencing reactions specific oligonucleotides complementary to the vector pGEM-T or primers complementary to GABA<sub>B</sub> receptor DNA were used.

The following primer combination gave PCR products corresponding to the 3'-end of the GABA<sub>B</sub> receptor cDNA: primer pairs 938 and 972; 938 and 973. Unexpectedly both these fragments lacked 149 base pairs, resulting in a frame shift and the insertion of a new termination codon. The following primer combination gave a PCR product corresponding to the 5'-part of the GABA<sub>B</sub> receptor 1a cDNA: 893 and 937. The primer pairs 1005 and 937, 1030 and 937 gave PCR products corresponding to the 5'-part of the GABA<sub>B</sub> receptor 1b cDNA. Also these PCR fragments lacked the same 149 base pairs which resulted in a frame shift and the insertion of a new termination codon.

These results show that Jurkat cells contain mRNA encoding two new forms of the human GABA<sub>B</sub> receptor. These are designated GABA<sub>B</sub> receptor 1c (SEQ ID NO: 54 and 55) (comprising the same 5'-part as the GABA<sub>B</sub> receptor 1a) and GABA<sub>B</sub> receptor 1d (SEQ ID NO: 56 and 57) (comprising the same 5'-part as the GABA<sub>B</sub> receptor 1b). These two forms of the GABA<sub>B</sub> receptor do not contain any of the transmembrane regions and are therefore expected to be soluble forms of the receptor.

#### EXAMPLE 3B: Analysis of cDNA encoding human GABA<sub>B</sub> receptors from hippocampus

Messenger RNA from human hippocampus was obtained from Clontech (Palo Alto, USA) (catalogue #6578-1). First strand cDNA synthesis reactions were performed using the First-strand cDNA Synthesis kit from Amersham Pharmacia Biotech (Uppsala, Sweden). The

pd(N)<sub>6</sub> primer was used to prime the first-strand synthesis. The generated cDNA molecules were used as template in the PCR reactions described below.

Specific PCR primer was designed (Table 8) based on the sequences of the cDNAs  
5 encoding human GABA<sub>B</sub> receptors 1a and 1b.

TABLE 8

Primers used for RT-PCR on mRNA from human hippocampus

Nr	Species	Sequence 5' - 3'	SEQ ID NO
937	Human	CTGGTTCCTCCCAATGTG	40
938	Human	GACGCTTATCGAGCAGCTTC	41

10

cDNA fragments encoding parts of the human GABA<sub>B</sub> receptors were amplified directly by PCR using the designed primers with the generated cDNA molecules as templates. All PCR experiments were carried out using the Perkin Elmer Taq DNA polymerase with Gene Amp (Roche Molecular Systems Inc., NJ, USA) with the following PCR program: +94°C  
15 for 1 minute, +50°C for 30 seconds, +72°C for 3 minutes; +94°C for 1 minute, +54°C for 30 seconds, +72°C for 3 minutes repeated 44 times; and finally +72°C for 7 minutes. The primer combination 938 and 937 gave a PCR product which corresponded to the expected size of the GABA<sub>B</sub> receptor 1a and 1b cDNA but also a fragment a smaller size.

20 The PCR products were subcloned into the pGEM-T vector from Promega (Madison, USA). The inserts were subjected to nucleotide sequence analysis, the complete nucleotide sequence for all subclones were determined using a Thermo Sequenase dye terminator cycle sequencing pre-mix kit (Amersham Pharmacia Biotech, Uppsala, Sweden). As  
25 primers for sequencing reactions specific oligonucleotides complementary to the vector pGEM-T or primers complementary to the cDNA encoding the GABA<sub>B</sub> receptor were used.

The larger PCR fragment was found to correspond to the 3'-part of the GABA<sub>B</sub> receptor 1a and 1b cDNA and the smaller fragment which lacked 149 base pairs was found to  
30 correspond to the 3'-part of the GABA<sub>B</sub> receptors 1c and 1d cDNA identified in Example 3A.

**EXAMPLE 4: Cloning and sequencing of cDNA encoding canine GABA<sub>B</sub> receptor 1b**

5 cDNA encoding the canine GABA<sub>B</sub> receptor 1b is isolated in a similar manner as described in Example 2 for receptor 1a. PCR primers specifically designed to be complementary to the 5'-end of the cDNA encoding the rat and human GABA<sub>B</sub> receptor 1b, together with PCR primers complementary to the 3'-end of the cDNA encoding the canine GABA<sub>B</sub> receptor 1a, and mRNA prepared from a suitable canine tissue, are used.

10

**EXAMPLE 5: Cloning of cDNA encoding canine GABA<sub>B</sub> receptor 1c**

Total RNA from canine liver was prepared using the RNeasy Total RNA Purification  
15 Protocols (Quiagen GmbH, Germany). The first-strand cDNA synthesis was performed using the First-strand cDNA Synthesis kit from (Amersham Pharmacia Biotech, Uppsala, Sweden). The pd(N)<sub>6</sub> primer was used to prime the first -strand synthesis. The generated cDNA molecules were used as templates in the PCR reaction described below.

20 Specific PCR primers (Table 9) were designed based on the sequence of canine GABA<sub>B</sub> receptor 1a cDNA.

**TABLE 9**

Primers used in RT-PCR

25

Nr	Species	Sequence 5'-3'	SEQ ID NO
936	canine	CTACCGCGCAATGAACTCCTCGTC	42
954	canine	CCTTCTTCTCCTCCTTCTTAGTGA	43

cDNA fragments encoding parts of the canine GABA<sub>B</sub> receptor were amplified directly by PCR using canine specific primers. All PCR experiments were carried out using the Perkin Elmer Taq DNA polymerase with Gene Amp (Roche Molecular Systems Inc., NJ, USA)  
30 with the following PCR program: +95°C for 1 minute, +54°C for 30 seconds, +72°C for 3



minutes, repeated 44 times and finally +72°C for 7 minutes. The primer combination gave a PCR product with a size corresponding to the GABA<sub>B</sub> receptor 1a but also a fragment of smaller size indicating the presence of a GABA<sub>B</sub> receptor 1c.

- 5 The PCR products were subcloned into the pGEM-T vector from Promega (Madison, USA). The inserts were subjected to nucleotide sequence analysis, the complete nucleotide sequence for all subclones were determined using a Thermo Sequenase dye terminator cycle sequencing pre-mix kit (Amersham Pharmacia Biotech, Uppsala, Sweden). As primers for sequencing reactions specific oligonucleotides complementary to the vector  
10 pGEM-T were used.

The smaller fragment was shown to lack 149 base pairs. This deletion caused a frame shift and an insertion of a new termination codon, verifying the existence of a canine GABA<sub>B</sub> receptor 1c.

- 15 Complete cDNA sequence encoding the canine GABA<sub>B</sub> receptor 1c (SEQ ID NO: 58) was obtained by aligning the sequences of the fragments obtained in Example 2A, Example 2B and Example 5.

- 20 **EXAMPLE 6. Cloning, sequencing and organization of human GABA<sub>B</sub> receptor genomic fragments**

- To determine the structural organization and sequence of the human GABA<sub>B</sub> receptor gene,  
25 human genomic DNA libraries and human genomic DNA were screened and analyzed. Human genomic libraries were obtained from Clontech (Palo Alto, CA, USA). The libraries were constructed from female leukocyte DNA (catalog # HL1111J), cloned into λEMBL-3 vector. The average size of inserts are 16 kb and the number of independent clones are  $1.7 \times 10^6$ . Human genomic DNA was obtained from Clontech (catalog # 6550-1).  
30 In order to isolate recombinant phages containing exon and intron sequences of the human GABA<sub>B</sub> receptor gene, 48 individual bacterial plates with a diameter of 150 mm and approximately  $4 \times 10^4$  individual plaques per plate, were screened. The methods and

solutions used were as described in the Library Protocol Handbook: General Procedures for the Hybridization of Lambda Phage Libraries w/DNA Probes (Clontech) with some modifications as will be apparent from the following.

- 5 The experiment was carried out essentially as follows. The numbers are given per plate basis. A sample of the phage library diluted in 0.1 ml sterile lambda diluent was prepared in order to obtain an estimated titer of 40,000 pfu (plaque forming units). A 0.6 ml LB-medium culture of the *E. coli* host strain K802 (obtained from Clontech) was infected with 40000 pfu recombinant phages for 15 minutes at +37°C. The culture was then mixed with  
10 7 ml top agarose (6.5 g of agarose added per liter LB) and poured onto LB plates. The plates were incubated at +37°C for approximately 7 hours. The plates were then chilled at +4°C.

- Plaque hybridization experiments were as follows. Membrane filters, Colony/Plaque  
15 Screen (DuPont, Wilmington, DE, USA), were placed onto the top of the plates for 3 minutes. For denaturation of DNA the filters were removed and floated in 0.5 M NaOH on a plastic wrap for 2 minutes, with the plaque side up. This step was repeated once to ensure efficient denaturation. Following neutralization the membrane filters were placed in 1M Tris-HCl pH 7.5, two times 2 minutes and allowed to dry.

- 20 To obtain probes for DNA hybridization screening of the membrane filters, a GABA<sub>B</sub> receptor cDNA clone was digested with SacII and a 479 bp fragment (base pairs 573-1051 in the cDNA encoding human GABA<sub>B</sub> receptor 1a, SEQ ID NO: 48) was separated by agarose electrophoresis, excised and transferred to a polypropylene microcentrifuge tube.  
25 Additional probes were obtained by PCR amplification of various regions of the GABA<sub>B</sub> receptor cDNA (base pairs 68-486 and 2368-2863 in the cDNA encoding human GABA<sub>B</sub> receptor 1a, SEQ ID NO: 48). The isolated cDNA fragment was <sup>32</sup>P-labeled using Megaprime DNA labeling system (Amersham Pharmacia Biotech, Uppsala, Sweden) by the following procedure. Water was added at a ratio of 3 ml per gram of gel, and placed in  
30 a boiling water bath for 7 minutes to melt the gel and denature the DNA. A volume of DNA/agarose solution containing 25 ng of DNA was added to the labeling reaction, according to the supplier's instructions. Labeled nucleotides were removed from DNA

labeling reactions using MicroSpin™ G-50 Columns (Amersham Pharmacia Biotech, Uppsala, Sweden ).

5 The DNA hybridization reaction was performed under stringent conditions according to the method described below. The filter membranes were prehybridized at +65°C for at least 1 hour in a solution composed of 1% SDS, 1M NaCl, and 10% dextran sulfate using a hybridization oven (Hybaid Ltd, Ashford, UK). Following prehybridization a solution containing denatured herring sperm DNA of a final concentration of 100 µg/ml and the <sup>32</sup>P-labeled DNA probe at a concentration <10 ng/ml (for optimal signal to background  
10 ratio) was added to the prehybridization solution and the membrane filters were incubated at +65°C for 10-20 hours. Following the removal of the hybridization solution the membrane filters were first washed in a 2xSSC (0.3M NaCl, 0.03M Na-citrate), 1% SDS solution two times for 5 minutes at room temperature. In the next step, the membrane filters were incubated +60°C two times for 30 minutes each in the same solution. In a third  
15 step, the filters were washed two times at room temperature in 0.1xSSC. Finally, the membrane filters were placed on a sheet of filter paper with the DNA face up, and allowed to dry. The dried membrane filters were then exposed to X-ray films and autoradiographed.

20 Of the approximately  $2 \times 10^6$  individual plaques analyzed, four hybridizing plaques were detected and isolated. These three isolates were designated #GR1, #GR12, #GR13 and #GR41, respectively. After several rescreening experiments, the recombinant phage DNA was purified using Qiagen Lambda Midi Kit (Qiagen GmbH, Germany). The purified DNA was digested with SalI and the fragments representing the inserts were isolated by agarose electrophoresis.

25 The sizes of the inserts were approximately isolate #GR1, 12 kb, isolate #GR12, 12 kb; isolate #GR13, 16kb; and isolate #GR41, 19 kb. These fragments were cloned into SalI digested linearized pUC19, resulting in the plasmids pAM362 (isolate #GR1), pAM363 (isolate #GR12), pAM364 (isolate #GR13) and pAM365 (isolate #GR41). The inserts from  
30 the four plaques which hybridizes to the GABA<sub>B</sub> receptor cDNA probes were analyzed by PCR, restriction mapping and hybridization to <sup>32</sup>P-labeled DNA fragments representing various regions of the GABA<sub>B</sub> receptor gene.

The cloned fragments in the plasmids pAM362, pAM363, pAM364 and pAM365 were characterized by restriction enzyme mapping, using EcoRI, HindIII, PstI, and BamHI. The approximate positions of the exons and the approximate size of the introns were analyzed and determined by PCR-based exon-exon linking and agarose gel electrophoresis.

In order to facilitate nucleotide sequence analysis, 7 restriction sub-fragments derived from pAM364, 2 restriction fragments derived from pAM362, and 1 restriction sub-fragment derived from pAM365 were isolated and cloned into pUC19, resulting in the plasmids pAM366-pAM375. The following strategy was employed; by combining PCR primers located within the pUC19 sequence either upstream or downstream of the cloning site, with a PCR primer with defined orientation and specific for the GABA<sub>B</sub> receptor derived subcloned fragment allowed the determination.

The inserts in the 10 plasmids pAM366-pAM375 were subjected to nucleotide sequence analysis. The nucleotide sequences for all subclones were determined using a Thermo Sequenase dye terminator cycle sequencing pre-mix kit (Amersham Pharmacia Biotech, Uppsala, Sweden). As primers for sequencing reactions specific oligonucleotides complementary to pUC19 or primers complementary to the GABA<sub>B</sub> receptor cDNA were used.

The genomic fragments cloned in the plasmids pAM362-pAM365 were shown to contain the complete transcribed part of the human GABA<sub>B</sub> receptor gene and extends > 3kb upstream of the first exon and > 2kb downstream of the last exon. The fragments cloned in the plasmid pAM362 were shown to contain exons 7-11, pAM363 exons 12-22, pAM364 exons 1-11, and pAM365 exons 12-23 of the GABA<sub>B</sub> receptor gene (Figure 1). The sequence of exons 1-11 and introns 1-10 is listed in SEQ ID NO: 60 and the sequence of exons 12-23 and introns 12-22 is listed in SEQ ID NO: 61.

The human GABA<sub>B</sub> receptor gene consists of 23 exons and 22 introns (Figure 1). The size of the exons range between 21 bp and 1486 bp. As can be noted from Table 10 exon/intron boundaries are in accordance with the AG/GT rule and conform well to the consensus sequence suggested by Mount et al. 1982.

TABLE 10

Exon-Intron boundaries of the GABA<sub>B</sub> receptor gene, sequences at exon-intron junctions.

		5' splice donor	3' splice acceptor	
Exon 1-Exon 2	CGAG	<u>GTAAGAG</u> .....	..... <u>CCGCCTCTCACTTAG</u>	ATGT
Exon 2-Exon 3	GAAG	<u>GTGCATC</u> .....	..... <u>CGACTCACCCCTTAG</u>	GTTG
Exon 3-Exon 4	TGTG	<u>GTGAGTA</u> .....	..... <u>CCWATCTCTCCACAG</u>	TCCG
Exon 4-Exon 5	CAGG	<u>GTGAGGG</u> .....	..... <u>CTTTCCTGCTGCCAG</u>	TGAA
Exon 5-Exon 6	TCAG	<u>GTGAGAT</u> .....	..... <u>CGCACCCCTCCTCAG</u>	AACG
Exon 6-Exon 7	CAAG	<u>GTAGCCC</u> .....	..... <u>CCTCTTGCTTTTCAG</u>	TGTG
Exon 7-Exon 8	TGTG	<u>GTAAGCA</u> .....	..... <u>CTCCCTGCCCCACAG</u>	CTTT
Exon 8-Exon 9	TTCG	<u>GTGAGGA</u> .....	..... <u>TTATTCCCACCCAAG</u>	ACTC
Exon 9-Exon10	GAAG	<u>GTCAGAT</u> .....	..... <u>CTTTCCTCTGTRGTAG</u>	CGCC
Exon10-Exon11	TGAG	<u>GTGGART</u> .....	..... <u>CTCCTCTGTATTCAG</u>	GTGT
Exon11-Exon12	CATG	<u>GTGAGAG</u> .....	..... <u>TTTTTTCCTCCCAAG</u>	ACAT
Exon12-Exon13	CTCT	<u>GTGAGTT</u> .....	..... <u>TGTTCTTCCCTCAG</u>	GGCC
Exon13-Exon14	CAGG	<u>GTTAGTA</u> .....	..... <u>TTGTCGTCTGCCCAG</u>	GTGG
Exon14-Exon15	ATTG	<u>GTGAGTG</u> .....	..... <u>CCCTGTGCCATGCAG</u>	GAGG
Exon15-Exon16	TCCG	<u>GTXAGTT</u> .....	..... <u>CCACCTCTGCCCTAG</u>	TTAT
Exon16-Exon17	CCAG	<u>GTGAGGA</u> .....	..... <u>TCTCTTCCTTCTAG</u>	GCCC
Exon17-Exon18	GAAG	<u>GTGAGCT</u> .....	..... <u>CACATATTTATCCAG</u>	ACTC
Exon18-Exon19	TGAG	<u>GTACCAC</u> .....	..... <u>TYGTTTCTGCCCTAG</u>	ACAT
Exon19-Exon20	CTTG	<u>GTGTGTG</u> .....	..... <u>CTCCTGCCATCCTAG</u>	GCAT
Exon20-Exon21	GGCA	<u>GTGAGCA</u> .....	..... <u>TGTCTTTCCTCTAG</u>	GTCC
Exon21-Exon22	CAAG	<u>GTAAGGA</u> .....	..... <u>AACATTTGCCCCAG</u>	ATGC
Exon22-Exon23	TGAG	<u>GTGCGGG</u> .....	..... <u>TGCTTCTTCTCCAG</u>	AAAG

5

A comparison of the sequences of the different forms of the human GABA<sub>B</sub> receptor cDNA (SEQ ID NO: 48, 50, 54, and 56) and the sequence of the human GABA<sub>B</sub> gene (SEQ ID NO: 60 and 61) reveals that different mRNA encoding human GABA<sub>B</sub> receptors are formed by alternative splicing. The translational start of the GABA<sub>B</sub> receptor 1a is localized in exon 2 and the translational stop is localized in exon-23. The mRNA encoding GABA<sub>B</sub> receptor 1b is formed by alternative splicing where part of intron 5 is retained together with exon 6 where the translational start of the GABA<sub>B</sub> receptor 1b is derived from the intron sequence. The mRNA encoding GABA<sub>B</sub> receptor 1c is formed by alternative splicing where exon 15 are removed together with introns 14 and 15 and a frame shift and a translational stop are generated in the sequence corresponding to exon 16.

15

The mRNA encoding GABA<sub>B</sub> receptor 1d is formed when the translational start of the GABA<sub>B</sub> receptor 1b is generated together with the translational stop of the GABA<sub>B</sub> receptor 1c.

- 5 The 1a isoform is formed by splicing exon 5 to a cryptic splice site in the middle of exon 6. Transcription of 1b isoform mRNA is most likely initiated from regulatory elements in intron 5. The ATG initiating translation of 1b mRNA is located in the 5'-end of exon 6.

- Additional variants of the mRNA encoding variants of the human GABA<sub>B</sub> receptor can be  
10 derived by alternative splicing where one or more of the exons or part of exons are excised in the processing of the pre-mRNA. The subsequent transcription of these mRNA will give rise to variants of the human GABA<sub>B</sub> receptor with potentially different biological and/or pharmacological activities.

15

EXAMPLE 7. Analysis of cDNA encoding human GABA<sub>B</sub> receptors from human brain

- Messenger RNA from human fetal brain (catalog #6525-1) and adult human brain (catalog #6516-1) were obtained from Clontech (Palo Alto, CA, USA). First strand cDNA synthesis  
20 reactions were performed using the first strand cDNA Synthesis kit from Amersham Pharmacia Biotech (Uppsala, Sweden). The pd(N)<sub>6</sub> primer was used to prime the first-strand synthesis. The generated cDNA molecules were used as templates in the PCR reactions described below.

- 25 Specific PCR primers was designed (Table 11 ) based on the sequences of the rat GABA<sub>B</sub> receptor 1a and 1b cDNA and human GABA<sub>B</sub> receptor 1a and 1b cDNA

TABLE 11

Primers used for RT-PCR on mRNA from human fetal brain

Nr	Species	Sequence 5'-3'	SEQ ID NO
838	Rat	ATGCGCGCCGGCAGCCAACATGCTGCTGCTGCTGGTGCCTCTCTTCC	62
863	Rat	GGTCATCCAGCGTTGAGGTGAAGAC	63
864	Rat	GAAGGTGCCAGATTATACATCCGC	64
865	Rat	CCACGATGATTCGAGCATCTTGACG	65
937	Human	CTGGTTCCTCCAATGTG	66
1015	Human	CCAGTGGACTATGAGATTGAG	67

- 5 cDNA fragments encoding parts of the human GABA<sub>B</sub> receptors were amplified directly by PCR using the designed primers with the generated cDNA molecules as templates. PCR experiments with primers 838, 863, 864 and 865 were carried out using the Perkin Elmer Taq DNA polymerase with Gene Amp (Roche Molecular System Inc., NJ, USA) with the following PCR program: +95°C for 1 minute, +50°C for 30 seconds, +72°C for 3 minutes, repeated 44 times and finally +72°C for 7 minutes. PCR experiments with primers 937 and 1015 were carried out using the Expand Long Template PCR System (Boehringer Mannheim GmbH, Germany) with the following PCR program: +94°C for 2 minutes; +94°C for 10 seconds, +55°C for 30 seconds, +68°C for 3 minutes repeated 35 times; and finally +68°C for 7 minutes. The primer combinations 838 and 863, 864 and 863, 864 and 865, 937 and 1015 gave PCR products.

The PCR products were subcloned into the pGEM-T vector from Promega (Madison, WI, USA). The inserts were subjected to nucleotide sequence analysis. The complete nucleotide sequence for all subclones were determined using a ThermoSequenase dye terminator cycle sequencing pre-mix kit (Amersham Pharmacia Biotech, Uppsala, Sweden). As for primers for sequencing reactions specific oligonucleotides complementary to the vector pGEM-T or primers complementary to the cDNA encoding the GABA<sub>B</sub> receptor were used.

A number of analyzed clones isolated from fetal brain were found to lack 186 base pairs, corresponding to exon 4. This alternative splicing resulted in a cDNA (SEQ ID NO: 70)

encoding a protein (SEQ ID NO: 71) comprising of 899 amino acids and designated GABA<sub>B</sub> receptor 1e.

Other clones from fetal brain lacked 368 base pairs, corresponding to exons 4, 5 and 6,  
5 resulting in a cDNA (SEQ ID NO: 72) where a frame shift and a translational stop codon are generated in the sequence corresponding to exon 7, encoding a protein (SEQ ID NO: 73) comprising only 97 amino acids designated GABA<sub>B</sub> receptor 1f.

One clone lacked 207 base pairs, corresponding to exons 4 and 5, resulting in a cDNA  
10 (SEQ ID NO: 74) encoding a protein (SEQ ID NO: 75) comprising 892 amino acids designated GABA<sub>B</sub> receptor 1g.

Another clone had two deletions, the first comprising 186 base pairs corresponding to exon 4, the second comprising 39 base pairs corresponding to part of exon 6, resulting in a  
15 cDNA (SEQ ID NO: 76) encoding a protein (SEQ ID NO: 77) comprising 886 amino acids designated GABA<sub>B</sub> receptor 1h.

Yet another clone from adult human brain was found to have a long deletion comprising 1194 base pairs corresponding to base pairs 319 - 1512 of the cDNA encoding human  
20 GABA<sub>B</sub> receptor 1a. This deletion corresponds to part of exon 4, exons 5-11, and part of exon 12. This cDNA (SEQ ID NO: 78) encodes a protein (SEQ ID NO: 79) comprising 563 amino acids designated GABA<sub>B</sub> receptor 1i.

One clone isolated from fetal brain lacked 284 base pairs corresponding to part of exon 3  
25 and the whole exon 4, generating a frame shift and a translational stop codon in the sequence corresponding to exon 5. This cDNA (SEQ ID NO: 80) encodes a protein (SEQ ID NO: 81) comprising only 105 amino acids designated GABA<sub>B</sub> receptor 1j.

30 **EXAMPLE 8. Analysis of cDNA encoding human GABA<sub>B</sub> receptors from Jurkat cells**

A guanidinisothiocyanate/CsCl method was used to isolate total RNA from Jurkat cells. First strand cDNA synthesis reactions were performed using the first strand cDNA



Synthesis kit from Amersham Pharmacia Biotech (Uppsala, Sweden). The pd(N)<sub>6</sub> primer was used to prime the first-strand synthesis. The generated cDNA molecules were used as templates in the PCR reactions described below.

- 5 Specific PCR primers was designed (Table 12) based on the sequences of the human GABA<sub>B</sub> receptor 1a and 1b cDNA

TABLE 12

Primers used for RT-PCR on mRNA from Jurkat cells

10

Nr	Species	Sequence 5'-3'	SEQ ID NO
937	Human	CTGGTTCCTCCCAATGTG	68
1015	Human	CCAGTGGACTATGAGATTGAG	69

- cDNA fragments encoding parts of the human GABA<sub>B</sub> receptors were amplified directly by PCR using the designed primers with the generated cDNA molecules as templates. The PCR experiment was carried out using the Expand Long Template PCR System (Boehringer Mannheim GmbH, Germany) with the following PCR program: +94°C for 2 minutes; +94°C for 10 seconds, +55°C for 30 seconds, +68°C for 3 minutes repeated 35 times; and finally +68°C for 7 minutes. The primer combination 937 and 1015 gave a PCR product.
- 15
- 20 The PCR products were subcloned into the pGEM-T vector from Promega (Madison, WI, USA). The inserts were subjected to nucleotide sequence analysis. The complete nucleotide sequence for all subclones were determined using a ThermoSequenase dye terminator cycle sequencing pre-mix kit (Amersham Pharmacia Biotech, Uppsala, Sweden). As for primers for sequencing reactions specific oligonucleotides complementary to the vector pGEM-T or
- 25 primers complementary to the cDNA encoding the GABA<sub>B</sub> receptor were used.

- Two clones had two deletions, the first comprising 368 base pairs corresponding to exons 4, 5 and 6, the second comprising 151 base pairs corresponding to exon 15 where a frame shift and a translational stop codon are generated in the sequence corresponding to exon 7.
- 30 This cDNA (SEQ ID NO: 82) encodes a protein (SEQ ID NO: 83) comprising only 98

amino acids designated GABA<sub>B</sub> receptor 1k which is identical to the GABA<sub>B</sub> receptor 1f described above.

Another two clones also had two deletions, the first comprising 246 base pairs

- 5 corresponding to part of exon 4, exon 5 and exon 6, the second comprising 149 base pairs corresponding to exon 15, generating a frame shift and a translational stop codon in the sequence corresponding to exon 16. This cDNA (SEQ ID NO: 84) encodes a protein (SEQ ID NO: 5) comprising 496 amino acids designated GABA<sub>B</sub> receptor 1l.

- 10 Additional variants of cDNA encoding the human GABA<sub>B</sub> receptors can be identified in a similar manner using PCR primers based on the sequence of the cDNA and genomic fragments encoding the human GABA<sub>B</sub> receptors disclosed in the present application.

The biological activity of these variants of the human GABA<sub>B</sub> receptor can be evaluated by  
15 transfection of suitable host cells with expression vectors comprising the corresponding cDNA sequences and subsequent measurement of binding of labeled ligands or activation of the receptor or modulation of receptor function.

20 **EXAMPLE 9: Generation of antibodies**

Antibodies were raised in rabbits against four different BSA-conjugated 20 amino acids long synthetic peptides corresponding to selected regions of the human and canine GABA<sub>B</sub> receptor extracellular domain. Two were directed against a sequence common for GABA<sub>B</sub>  
25 receptor 1a and b (ab1 and ab2), one against a GABA<sub>B</sub> receptor 1a-specific region (a1) and one against a GABA<sub>B</sub> receptor 1b-specific sequence (b1). To allow BSA-conjugation, a cystein residue was added to the N-terminus in all peptides but a1, which contains an endogenous cystein.

- 30 Peptide a1: (SEQ ID NO: 49 amino acids 18-37)

Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile Ile His Pro Pro Trp

Peptide ab1: (SEQ ID NO: 49 amino acids 197-216 with N-terminally added Cys)

Cys - Glu Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp Tyr Glu Leu Lys Leu Ile  
His His

5 Peptide ab2: (SEQ ID NO: 49 amino acids 271-290 with N-terminally added Cys)

Cys - Ser Pro Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro  
Ser Ala

Peptide b1: (SEQ ID NO: 57 amino acids 30-47 with N-terminally added Cys)

10 Cys - Ser His Ser Pro His Leu Pro Arg Pro His Ser Arg Val Pro Pro His Pro Ser

The antibodies were purified from rabbit serum by affinity chromatography using the  
corresponding immobilized peptide and subsequently used to detect expression of  
recombinant GABA<sub>B</sub> receptor isoforms on Western blots.

15

#### EXAMPLE 10: Heterologous expression of GABA<sub>B</sub> receptor isoforms in mammalian cells

A HindIII / SalI cDNA fragment encoding the human GABA<sub>B</sub> receptor 1b isoform was  
20 cloned into a BPV (bovine papilloma virus)-based expression vector containing the mMT-  
1 (murine metallothioneine) promoter. Using the calcium phosphate method, murine C127  
cells were co-transfected with the GABA<sub>B</sub> receptor expression construct and an expression  
plasmid containing a G418 resistance marker gene using the calcium phosphate method.  
G418 resistant clones were evaluated by Western blot analysis for expression of the  
25 approximately 100 kDa GABA<sub>B</sub> receptor 1b isoform (Figure 2). Similarly, but using  
Lipofectamine (Life Technologies Inc, Rockville, MD, USA) for transfection, the human  
GABA<sub>B</sub> receptor 1b isoform was expressed in human HEK-293 cells using the pCI-neo  
expression vector. The identity of the heterologously expressed receptor was verified in  
HEK-293 cells by Western blot analysis and radioligand binding experiments.

30

A cDNA fragment encoding the human GABA<sub>B</sub> receptor 1d isoform was cloned into a  
BPV-based expression vector containing the mMT-1 promoter. Using the calcium  
phosphate method, murine C127 cells were co-transfected with the GABA<sub>B</sub> receptor

expression construct and an expression plasmid containing a G418 resistance marker gene. G418 resistant clones, and concentrated medium from the same clones, were evaluated for GABA<sub>B</sub> receptor 1d isoform expression by Western blot analysis (Figure 3). The experiment revealed the human GABA<sub>B</sub> receptor 1d to be a secreted isoform.

5

**EXAMPLE 11: Heterologous expression of GABA<sub>B</sub> receptor isoforms in *E. coli***

A cDNA fragment encoding the human GABA<sub>B</sub> receptor 1d isoform was cloned into a modified pET (Pharmacia Amersham, Uppsala, Sweden) vector downstream of a STII (heat stable enterotoxin II of *E. coli*) signal peptide and followed by a thrombin cleavage site and a hexahistidine tag. The expression construct was subsequently used to transform the BL21 (DE3) *E. coli* strain. Western blot analysis of IPTG-induced bacteria revealed expression of a human GABA<sub>B</sub> receptor 1d isoform of expected size (Figure 4).

15

In addition, the human GABA<sub>B</sub> receptor 1d isoform was successfully expressed without fusion to a bacterial signal peptide in *E. coli* strain AD494 (DE3).

**EXAMPLE 12: Method for the screening of substances which are GABA<sub>B</sub> receptor antagonists or agonists**

GABA<sub>B</sub> receptor expressing cells, transgenic animals or cells and tissues derived thereof, are used to screen substance libraries for antagonist or agonist activities. Screening is performed as ligand binding assays or functional assays. For screening, cells and tissues are prepared in various ways, each uniquely suited to its purpose. Ligand binding assays are performed *in vivo* or *in vitro*. Functional assays exemplified by, but not limited to, Ca<sup>++</sup>-responses, cAMP-responses and effects on Cl<sup>-</sup> and K<sup>+</sup> channels, are performed in living cells, broken cells, isolated cell membranes, as well as in tissues and in living animals.

## CLAIMS

1. A nucleic acid molecule encoding a human or canine GABA<sub>B</sub> receptor, or a functionally equivalent modified form thereof.  
5
2. A nucleic acid molecule according to claim 1 encoding a human GABA<sub>B</sub> receptor, or a functionally equivalent modified form thereof.
3. A nucleic acid molecule according to claim 2 encoding the human GABA<sub>B</sub> receptor  
10 1a, or a functionally equivalent modified form thereof.
4. A nucleic acid molecule according to claim 3 selected from:  
(a) a nucleic acid molecule comprising a nucleotide sequence set forth as SEQ ID NO: 48;  
15 (b) a nucleic acid molecule comprising a nucleotide sequence capable of hybridizing, under stringent hybridization conditions, to a nucleotide sequence complementary to the polypeptide coding region of a DNA molecule as defined in (a); and  
(c) a nucleic acid molecule comprising a nucleotide sequence which is degenerate as a result of the genetic code to a nucleotide sequence as defined in (a) or (b).  
20
5. A nucleic acid molecule according to claim 2 encoding the human GABA<sub>B</sub> receptor 1b, or a functionally equivalent modified form thereof..
6. A nucleic acid molecule according to claim 5 selected from:  
25 (a) nucleic acid molecules comprising a nucleotide sequence set forth as SEQ ID NO: 50;  
(b) nucleic acid molecules comprising a nucleotide sequence capable of hybridizing, under stringent hybridization conditions, to a nucleotide sequence complementary the polypeptide coding region of a DNA molecule as defined in (a); and  
30 (c) nucleic acid molecules comprising a nucleotide sequence which is degenerate as a result of the genetic code to a nucleotide sequence as defined in (a) or (b).

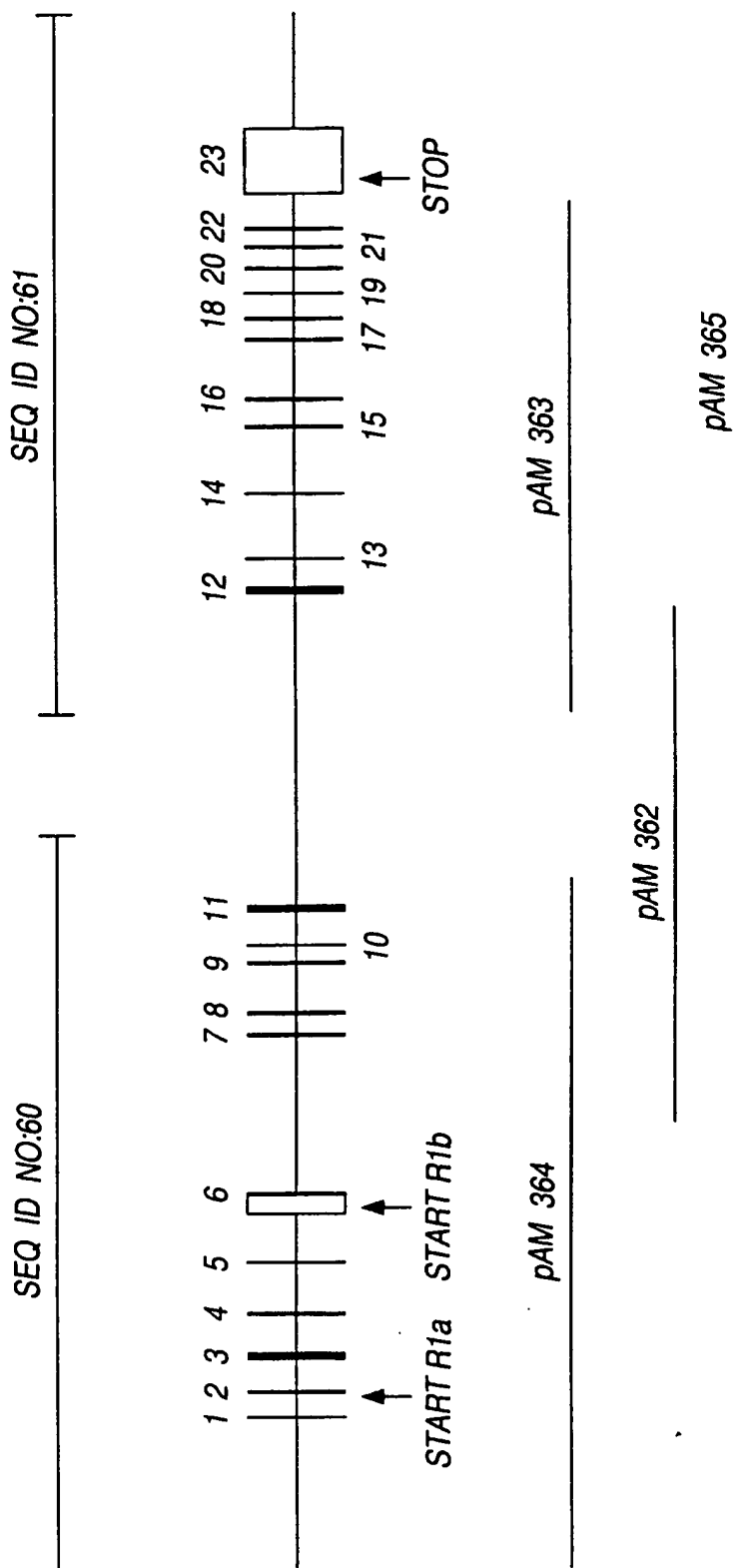
7. A nucleic acid molecule according to claim 2 encoding the human GABA<sub>B</sub> receptor 1c, or a functionally equivalent modified form thereof.
8. A nucleic acid molecule according to claim 7 selected from:
- 5 (a) nucleic acid molecules comprising a nucleotide sequence set forth as SEQ ID NO: 54;
- (b) nucleic acid molecules comprising a nucleotide sequence capable of hybridizing, under stringent hybridization conditions, to a nucleotide sequence complementary the polypeptide coding region of a DNA molecule as defined in (a); and
- 10 (c) nucleic acid molecules comprising a nucleotide sequence which is degenerate as a result of the genetic code to a nucleotide sequence as defined in (a) or (b).
9. A nucleic acid molecule according to claim 2 encoding the human GABA<sub>B</sub> receptor 1d, or a functionally equivalent modified form thereof..
- 15 10. A nucleic acid molecule according to claim 9 selected from:
- (a) nucleic acid molecules comprising a nucleotide sequence set forth as SEQ ID NO: 56;
- (b) nucleic acid molecules comprising a nucleotide sequence capable of hybridizing,
- 20 under stringent hybridization conditions, to a nucleotide sequence complementary the polypeptide coding region of a DNA molecule as defined in (a); and
- (c) nucleic acid molecules comprising a nucleotide sequence which is degenerate as a result of the genetic code to a nucleotide sequence as defined in (a) or (b).
- 25 11. A nucleic acid molecule according to claim 1 encoding a canine GABA<sub>B</sub> receptor, or a functionally equivalent modified form thereof.
12. A nucleic acid molecule according to claim 11 encoding the canine GABA<sub>B</sub> receptor 1a, or a functionally equivalent modified form thereof.
- 30 13. A nucleic acid molecule according to claim 12 selected from

- (a) nucleic acid molecules comprising a nucleotide sequence set forth as SEQ ID NO: 52;
- (b) nucleic acid molecules comprising a nucleotide sequence capable of hybridizing, under stringent hybridization conditions, to a nucleotide sequence complementary the polypeptide coding region of a DNA molecule as defined in (a); and
- (c) nucleic acid molecules comprising a nucleotide sequence which is degenerate as a result of the genetic code to a nucleic acid sequence as defined in (a) or (b).
- 14 A nucleic acid molecule according to claim 11 encoding the canine GABA<sub>B</sub> receptor 1c, or a functionally equivalent modified form thereof.
15. A nucleic acid molecule according to claim 14 selected from
- (a) nucleic acid molecules comprising a nucleotide sequence set forth as SEQ ID NO: 58;
- (b) nucleic acid molecules comprising a nucleotide sequence capable of hybridizing, under stringent hybridization conditions, to a nucleotide sequence complementary the polypeptide coding region of a DNA molecule as defined in (a); and
- (c) nucleic acid molecules comprising a nucleotide sequence which is degenerate as a result of the genetic code to a nucleic acid sequence as defined in (a) or (b).
16. A recombinant polypeptide encoded by a nucleotide sequence according to any one of claims 1 to 15.
17. The polypeptide according to claim 16 comprising an amino acid sequence set forth as SEQ ID NO: 49, 51, 53, 55, 57 or 59 in the Sequence Listing.
18. A polypeptide according to claim 16 which has been posttranslationally modified.
19. A vector transformed with a nucleic acid molecule according to any one of claims 1 to 15.
20. A cultured host cell harboring a vector according to claim 19.

21. A process for the production of a GABA<sub>B</sub> receptor, said process comprising culturing a host cell according to claim 20 under conditions whereby the said polypeptide is produced, and recovering the said polypeptide.
- 5
22. A method for the screening of compounds which are inhibitors of transient lower esophageal sphincter relaxations, said method comprising the use of a nucleic acid molecule encoding a GABA<sub>B</sub> receptor.
- 10 23. A method according to claim 22 wherein the said nucleic acid molecule encoding a GABA<sub>B</sub> receptor is the nucleic acid molecule according to any one of claims 1 to 15.
24. A method for the screening of compounds which are agonists or antagonists to a GABA<sub>B</sub> receptor, said method comprising the use of a nucleic acid molecule
- 15 according to any one of claims 1 to 15.
25. A method according to any one of claims 22 to 24 comprising the steps (a) transforming a cultured cell with a nucleic acid molecule encoding a GABA<sub>B</sub> receptor, so that a GABA<sub>B</sub> receptor is expressed on the surface of the cell; (b)
- 20 contacting a test compound with the said cell; and (c) determining whether the test compound binds to, and/or activate, the GABA<sub>B</sub> receptor.
26. A pharmaceutical compositions comprising a soluble GABA<sub>B</sub> receptor further comprising one or more pharmaceutical acceptable carriers and/or diluents.



1/2



1kb

Fig.1

2/2

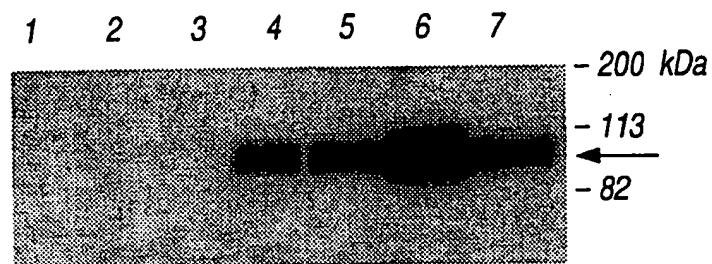


Fig.2

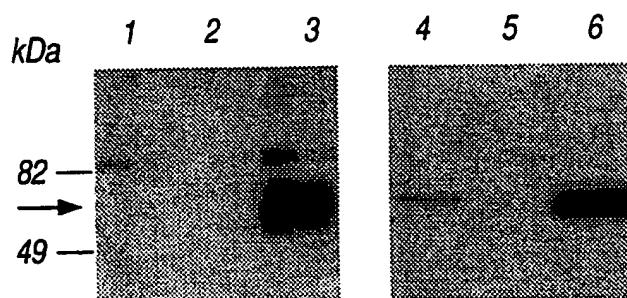


Fig.3

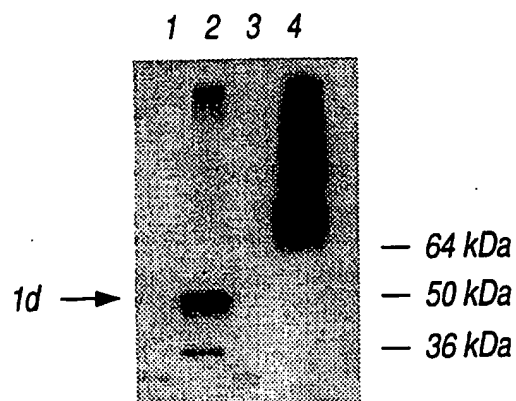


Fig.4

## SEQUENCE LISTING

5

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

- (A) NAME: ASTRA AB  
10 (B) STREET: Västra Mälarehamnen 9  
(C) CITY: Södertälje  
(E) COUNTRY: Sweden  
(F) POSTAL CODE (ZIP): S-151 85  
(G) TELEPHONE: +46-8-553 260 00  
15 (H) TELEFAX: +46-8-553 288 20  
(I) TELEX: 19237 astra s

(ii) TITLE OF INVENTION: New nucleotide sequences

20 (iii) NUMBER OF SEQUENCES: 85

## (iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

## (2) INFORMATION FOR SEQ ID NO: 1:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

40

GTTTCTTCTC GGATCCAGCT GTGCCTG

27

## (2) INFORMATION FOR SEQ ID NO: 2:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

15 CAGGCACAGC TGGATCCGAG AAGAAACT

28

## (2) INFORMATION FOR SEQ ID NO: 3:

- 20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

30 CGGTCGACTC ACTTGTAAG CAAATGTACT CGACTCCC

38

## (2) INFORMATION FOR SEQ ID NO: 4:

- 35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 41 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ATGCGCGCCG GCAGCCAACA TGCTGCTGCT GCTGCTGGTG C

41

5 (2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CGGTCGACTC ACTTGTAAG CAAATGTACT CGACTCCCAT CACAGC

46

20 (2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

25 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

ATGCGCGCCG GCAGCCAACA TGCTGCTGCT GCTGCTGGTG CCTCTCTTCC

50

35 (2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

40 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CAGGCACAGC TGGATCCGAG AAGAACTCT GTCGGAAAGT

40

5

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GGTCATCCAG CGTTGAGGTG AAGAC

25

20

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GAAGGTTGCC AGATTATACA TCCGC

25

35

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

5

CCACGATGAT TCGAGCATCT TGACG

25

(2) INFORMATION FOR SEQ ID NO: 11:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

15

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

20

GCCTCTCACT CCCCTCATCT CC

22

(2) INFORMATION FOR SEQ ID NO: 12:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

30

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

35

GAGTGAAGGA GGCTGGAATT G

21

(2) INFORMATION FOR SEQ ID NO: 13:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GACGCTTATC GAGCAGCTTC

20

10

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

AGCCCAGAAC TCACAGGGGG ACAT

24

25

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GCTTCAAGCC AGGTACGAAC TAA

23

40

(2) INFORMATION FOR SEQ ID NO: 16:



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

TGGCCCTCCA CCGCCTCAGT CATCTCA

27

## (2) INFORMATION FOR SEQ ID NO: 17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CCATCCTAAT ACGACTCACT ATAGGGC

27

## (2) INFORMATION FOR SEQ ID NO: 18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

CTCAATCTCA TAGTCCACTG G

21

## (2) INFORMATION FOR SEQ ID NO: 19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

CCTTGAGGCC CGGGGAGAG

19

## (2) INFORMATION FOR SEQ ID NO: 20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

CAGGCACAGC TGGATCCGAG AAGAAACT

28

## (2) INFORMATION FOR SEQ ID NO: 21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CGGTCGACTC ACTTGTAAG CAAATGTACT CGACTCCCAT CACAGC

46

## (2) INFORMATION FOR SEQ ID NO: 22:

- 5 (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 50 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

15 ATGCGCGCCG GCAGCCAACA TGCTGCTGCT GCTGCTGGTG CCTCTCTTCC

50

## (2) INFORMATION FOR SEQ ID NO: 23:

- 20 (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 22 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

30 CGTCAAGATG CTCGAATCAT CG

22

## (2) INFORMATION FOR SEQ ID NO: 24:

- 35 (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

CAGGGGGCTC AGAGGGTCCC

20

## 5 (2) INFORMATION FOR SEQ ID NO: 25:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

CAGGCACAGC TGGATCCGAG AAGAACTCT GTCGGAAAGT

40

## 20 (2) INFORMATION FOR SEQ ID NO: 26:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

25 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

CGGTCGACTC ACTTGTAAG CAAATGTACT CGACTCCCAT CACAGCTAAG

50

## 35 (2) INFORMATION FOR SEQ ID NO: 27:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

40 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

ACTTTCCGAC AGAGTTTCTT CTCGGATCCA GCTGTGCCTG

40

5

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

CCACGATGAT TCGAGCATCT TGACG

25

20

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

CTACCGCGCA ATGAACTCCT CGTC

24

35

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

5

CGAGGTGGCG TTGGGGTCT GTGC

24

(2) INFORMATION FOR SEQ ID NO: 31:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

15

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

20

CCATCCTAAT ACGACTCACT ATAGGGC

27

(2) INFORMATION FOR SEQ ID NO: 32:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

30

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

35

ACTCACTATA GGGCTCGAGC GGC

23

(2) INFORMATION FOR SEQ ID NO: 33:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

GACGCTTATC GAGCAGCTTC

20

10

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

15

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

AGCCCAGAAC TCACAGGGGG ACAT

24

25

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

30

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

GCTTCAAGCC AGGTACGAAC TAA

23

40

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

10 GGAGCACCCC CAAGCCCCAC TG

22

(2) INFORMATION FOR SEQ ID NO: 37:

- 15 (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

25 CTGGTTCCTC CCAATGTG

18

(2) INFORMATION FOR SEQ ID NO: 38:

- 30 (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

40 CCTCTCACTC CCCTCATCTC

20<sub>0</sub>

(2) INFORMATION FOR SEQ ID NO: 39:



- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 22 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

AAGCCAACCT TCCCTGCTTC TC

22

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 18 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

CTGGTTCCTC CCAATGTG

18

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GACGCTTATC GAGCAGCTTC

20

## (2) INFORMATION FOR SEQ ID NO: 42:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## 10 (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

15 CTACCGCGCA ATGAACTCCT CGTC 24

## (2) INFORMATION FOR SEQ ID NO: 43:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## 25 (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

30 CCTTCTTCTC CTCCTTCTTA GTGA 24

## (2) INFORMATION FOR SEQ ID NO: 44:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 2883 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## 40 (ii) MOLECULE TYPE: cDNA to mRNA

## (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Rattus norvegicus*

5

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..2883

10

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Kaupmann, K

Huggel, K

Heid, J

Flor, P

15

Bischoff, S

Mickel, S

McMaster, G

Angst, C

Bittiger, H

20

Froestl, W

(B) TITLE: Expression cloning of GABA-B receptors  
uncovers similarity to metabotropic glutamate  
receptors

(C) JOURNAL: Nature

25

(D) VOLUME: 386

(F) PAGES: 239-246

(G) DATE: 20 march-1997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

30

ATG CTG CTG CTG CTG CTG GTG CCT CTC TTC CTC CGC CCC CTG GGC GCT 48

Met Leu Leu Leu Leu Leu Val Pro Leu Phe Leu Arg Pro Leu Gly Ala

1

5

10

15

35

GGC GGC GGC CAG ACC CCC AAC GCC ACC TCG GAA GGT TGC CAG ATT ATA 96

Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile Ile

20

25

30

CAT CCG CCC TGG GAA GGT GGC ATC AGG TAC CGT GGC TTG ACT CGC GAC 144

40

His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg Asp

35

40

45

CAG GTG AAG GCC ATC AAC TTC CTG CCT GTG GAC TAT GAG ATC GAA TAT 192

	Gln	Val	Lys	Ala	Ile	Asn	Phe	Leu	Pro	Val	Asp	Tyr	Glu	Ile	Glu	Tyr	—
	50						55					60					
	GTG	TGC	CGA	GGG	GAG	CGC	GAG	GTG	GTG	GGG	CCC	AAG	GTG	CGC	AAA	TGC	240
5	Val	Cys	Arg	Gly	Glu	Arg	Glu	Val	Val	Gly	Pro	Lys	Val	Arg	Lys	Cys	
	65					70				75					80		
	CTG	GCC	AAC	GGC	TCC	TGG	ACG	GAT	ATG	GAC	ACA	CCC	AGC	CGC	TGT	GTC	288
10	Leu	Ala	Asn	Gly	Ser	Trp	Thr	Asp	Met	Asp	Thr	Pro	Ser	Arg	Cys	Val	
				85						90					95		
	CGA	ATC	TGC	TCC	AAG	TCT	TAT	TTG	ACC	CTG	GAA	AAT	GGG	AAG	GTT	TTC	336
	Arg	Ile	Cys	Ser	Lys	Ser	Tyr	Leu	Thr	Leu	Glu	Asn	Gly	Lys	Val	Phe	
				100					105					110			
15	CTG	ACG	GGT	GGG	GAC	CTC	CCA	GCT	CTG	GAT	GGA	GCC	CGG	GTG	GAG	TTC	384
	Leu	Thr	Gly	Gly	Asp	Leu	Pro	Ala	Leu	Asp	Gly	Ala	Arg	Val	Glu	Phe	
				115				120					125				
20	CGA	TGT	GAC	CCC	GAC	TTC	CAT	CTG	GTG	GGC	AGC	TCC	CGG	AGC	GTC	TGT	432
	Arg	Cys	Asp	Pro	Asp	Phe	His	Leu	Val	Gly	Ser	Ser	Arg	Ser	Val	Cys	
		130				135					140						
	AGT	CAG	GGC	CAG	TGG	AGC	ACC	CCC	AAG	CCC	CAC	TGC	CAG	GTG	AAT	CGA	480
25	Ser	Gln	Gly	Gln	Trp	Ser	Thr	Pro	Lys	Pro	His	Cys	Gln	Val	Asn	Arg	
	145				150					155				160			
	ACG	CCA	CAC	TCA	GAA	CGG	CGT	GCA	GTA	TAC	ATC	GGG	GCG	CTG	TTT	CCC	528
30	Thr	Pro	His	Ser	Glu	Arg	Arg	Ala	Val	Tyr	Ile	Gly	Ala	Leu	Phe	Pro	
				165						170				175			
	ATG	AGC	GGG	GGC	TGG	CCG	GGG	GGC	CAG	GCC	TGC	CAG	CCC	GCG	GTG	GAG	576
	Met	Ser	Gly	Gly	Trp	Pro	Gly	Gly	Gln	Ala	Cys	Gln	Pro	Ala	Val	Glu	
				180				185					190				
35	ATG	GCG	CTG	GAG	GAC	GTT	AAC	AGC	CGC	AGA	GAC	ATC	CTG	CCG	GAC	TAC	624
	Met	Ala	Leu	Glu	Asp	Val	Asn	Ser	Arg	Arg	Asp	Ile	Leu	Pro	Asp	Tyr	
		195				200					205						
40	GAG	CTC	AAG	CTT	ATC	CAC	CAC	GAC	AGC	AAG	TGT	GAC	CCA	GGG	CAA	GCC	672
	Glu	Leu	Lys	Leu	Ile	His	His	Asp	Ser	Lys	Cys	Asp	Pro	Gly	Gln	Ala	
		210				215					220						

	ACC AAG TAC TTG TAC GAA CTA CTC TAC AAT GAC CCC ATC AAG ATC ATT	720
	Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile Ile	
	225 230 235 240	
5	CTC ATG CCT GGC TGT AGT TCT GTC TCC ACA CTT GTA GCT GAG GCT GCC	768
	Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala	
	245 250 255	
	CGG ATG TGG AAC CTT ATT GTG CTC TCA TAT GGC TCC AGT TCA CCA GCC	816
10	Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala	
	260 265 270	
	TTG TCA AAC CGA CAG CGG TTT CCC ACG TTC TTC CGG ACG CAT CCA TCC	864
	Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro Ser	
15	275 280 285	
	GCC ACA CTC CAC AAT CCC ACC CGG GTG AAA CTC TTC GAA AAG TGG GGC	912
	Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp Gly	
	290 295 300	
20	TGG AAG AAG ATC GCT ACC ATC CAA CAG ACC ACC GAG GTC TTC ACC TCA	960
	Trp Lys Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr Ser	
	305 310 315 320	
25	ACG CTG GAT GAC CTG GAG GAG CGA GTG AAA GAG GCT GGG ATC GAG ATC	1008
	Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu Ile	
	325 330 335	
	ACT TTC CGA CAG AGT TTC TTC TCG GAT CCA GCT GTG CCT GTT AAA AAC	1056
30	Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys Asn	
	340 345 350	
	CTG AAG CGT CAA GAT GCT CGA ATC ATC GTG GGA CTT TTC TAT GAG ACG	1104
	Leu Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu Thr	
35	355 360 365	
	GAA GCC CGG AAA GTT TTT TGT GAG GTC TAT AAG GAA AGG CTC TTT GGG	1152
	Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly	
	370 375 380	
40	AAG AAG TAC GTC TGG TTC CTC ATC GGG TGG TAT GCT GAC AAC TGG TTC	1200
	Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe	
	385 390 395 400	

	AAG ACC TAT GAC CCG TCA ATC AAT TGT ACA GTG GAA GAA ATG ACC GAG	1248
	Lys Thr Tyr Asp Pro Ser Ile Asn Cys Thr Val Glu Glu Met Thr Glu	
	405 410 415	
5	GCG GTG GAG GGC CAC ATC ACC ACG GAG ATT GTC ATG CTG AAC CCT GCC	1296
	Ala Val Glu Gly His Ile Thr Thr Glu Ile Val Met Leu Asn Pro Ala	
	420 425 430	
10	AAC ACC CGA AGC ATT TCC AAC ATG ACG TCA CAG GAA TTT GTG GAG AAA	1344
	Asn Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu Lys	
	435 440 445	
	CTA ACC AAG CGG CTG AAA AGA CAC CCC GAG GAG ACT GGA GGC TTC CAG	1392
15	Leu Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln	
	450 455 460	
	GAG GCA CCA CTG GCC TAT GAT GCT ATC TGG GCC TTG GCT TTG GCC TTG	1440
	Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Leu	
20	465 470 475 480	
	AAC AAG ACG TCT GGA GGA GGT GGT CGT TCC GGC GTG CGC CTG GAG GAC	1488
	Asn Lys Thr Ser Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu Asp	
	485 490 495	
25	TTT AAC TAC AAC AAC CAG ACC ATT ACA GAC CAG ATC TAC CGG GCC ATG	1536
	Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala Met	
	500 505 510	
30	AAC TCC TCC TCC TTT GAG GGC GTT TCT GGC CAT GTG GTC TTT GAT GCC	1584
	Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val Val Phe Asp Ala	
	515 520 525	
	AGC GGC TCC CGG ATG GCA TGG ACA CTT ATC GAG CAG CTA CAG GGC GGC	1632
35	Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly Gly	
	530 535 540	
	AGC TAC AAG AAG ATC GGC TAC TAC GAC AGC ACC AAG GAT GAT CTT TCC	1680
	Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu Ser	
40	545 550 555 560	
	TGG TCC AAA ACG GAC AAG TGG ATT GGA GGG TCT CCC CCA GCT GAC CAG	1728
	Trp Ser Lys Thr Asp Lys Trp Ile Gly Gly Ser Pro Pro Ala Asp Gln	

	565	570	575	
	ACC TTG GTC ATC AAG ACA TTC CGT TTC CTG TCT CAG AAA CTC TTT ATC	1776		
	Thr Leu Val Ile Lys Thr Phe Arg Phe Leu Ser Gln Lys Leu Phe Ile			
5	580	585	590	
	TCC GTC TCA GTT CTC TCC AGC CTG GGC ATT GTT CTT GCT GTT GTC TGT	1824		
	Ser Val Ser Val Leu Ser Ser Leu Gly Ile Val Leu Ala Val Val Cys			
	595	600	605	
10	CTG TCC TTT AAC ATC TAC AAC TCC CAC GTT CGT TAT ATC CAG AAC TCC	1872		
	Leu Ser Phe Asn Ile Tyr Asn Ser His Val Arg Tyr Ile Gln Asn Ser			
	610	615	620	
15	CAG CCC AAC CTG AAC AAT CTG ACT GCT GTG GGC TGC TCA CTG GCA CTG	1920		
	Gln Pro Asn Leu Asn Asn Leu Thr Ala Val Gly Cys Ser Leu Ala Leu			
	625	630	635	640
	GCT GCT GTC TTC CCT CTC GGG CTG GAT GGT TAC CAC ATA GGG AGA AGC	1968		
20	Ala Ala Val Phe Pro Leu Gly Leu Asp Gly Tyr His Ile Gly Arg Ser			
	645	650	655	
	CAG TTC CCG TTT GTC TGC CAG GCC CGC CTT TGG CTC TTG GGC TTG GGC	2016		
	Gln Phe Pro Phe Val Cys Gln Ala Arg Leu Trp Leu Leu Gly Leu Gly			
25	660	665	670	
	TTT AGT CTG GGC TAT GGC TCT ATG TTC ACC AAG ATC TGG TGG GTC CAC	2064		
	Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr Lys Ile Trp Trp Val His			
	675	680	685	
30	ACA GTC TTC ACG AAG AAG GAG GAG AAG AAG GAG TGG AGG AAG ACC CTA	2112		
	Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp Arg Lys Thr Leu			
	690	695	700	
35	GAG CCC TGG AAA CTC TAT GCC ACT GTG GGC CTG CTG GTG GGC ATG GAT	2160		
	Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly Leu Leu Val Gly Met Asp			
	705	710	715	720
	GTC CTG ACT CTT GCC ATC TGG CAG ATT GTG GAC CCC TTG CAC CGA ACC	2208		
40	Val Leu Thr Leu Ala Ile Trp Gln Ile Val Asp Pro Leu His Arg Thr			
	725	730	735	
	ATT GAG ACT TTT GCC AAG GAG GAA CCA AAG GAA GAC ATC GAT GTC TCC	2256		

	Ile	Glu	Thr	Phe	Ala	Lys	Glu	Glu	Pro	Lys	Glu	Asp	Ile	Asp	Val	Ser	
				740					745						750		
	ATT	CTG	CCC	CAG	TTG	GAG	CAC	TGC	AGC	TCC	AAG	AAG	ATG	AAT	ACG	TGG	2304
5	Ile	Leu	Pro	Gln	Leu	Glu	His	Cys	Ser	Ser	Lys	Lys	Met	Asn	Thr	Trp	
				755				760					765				
	CTT	GGC	ATT	TTC	TAT	GGT	TAC	AAG	GGG	CTG	CTG	CTG	CTG	CTG	GGA	ATC	2352
10	Leu	Gly	Ile	Phe	Tyr	Gly	Tyr	Lys	Gly	Leu	Leu	Leu	Leu	Leu	Gly	Ile	
		770					775					780					
	TTT	CTT	GCT	TAC	GAA	ACC	AAG	AGC	GTG	TCC	ACT	GAA	AAG	ATC	AAT	GAC	2400
	Phe	Leu	Ala	Tyr	Glu	Thr	Lys	Ser	Val	Ser	Thr	Glu	Lys	Ile	Asn	Asp	
	785					790					795					800	
15																	
	CAC	AGG	GCC	GTG	GGC	ATG	GCT	ATC	TAC	AAT	GTC	GCG	GTC	CTG	TGT	CTC	2448
	His	Arg	Ala	Val	Gly	Met	Ala	Ile	Tyr	Asn	Val	Ala	Val	Leu	Cys	Leu	
					805					810					815		
20	ATC	ACT	GCT	CCT	GTG	ACC	ATG	ATC	CTT	TCC	AGT	CAG	CAG	GAC	GCA	GCC	2496
	Ile	Thr	Ala	Pro	Val	Thr	Met	Ile	Leu	Ser	Ser	Gln	Gln	Asp	Ala	Ala	
				820					825					830			
	TTT	GCC	TTT	GCC	TCT	CTG	GCC	ATC	GTG	TTC	TCT	TCC	TAC	ATC	ACT	CTG	2544
25	Phe	Ala	Phe	Ala	Ser	Leu	Ala	Ile	Val	Phe	Ser	Ser	Tyr	Ile	Thr	Leu	
		835						840					845				
	GTT	GTG	CTC	TTT	GTG	CCC	AAG	ATG	CGC	AGG	CTG	ATC	ACC	CGA	GGG	GAA	2592
	Val	Val	Leu	Phe	Val	Pro	Lys	Met	Arg	Arg	Leu	Ile	Thr	Arg	Gly	Glu	
30		850					855					860					
	TGG	CAG	TCT	GAA	ACG	CAG	GAC	ACC	ATG	AAA	ACA	GGA	TCA	TCC	ACC	AAC	2640
	Trp	Gln	Ser	Glu	Thr	Gln	Asp	Thr	Met	Lys	Thr	Gly	Ser	Ser	Thr	Asn	
	865					870					875					880	
35																	
	AAC	AAC	GAG	GAA	GAG	AAG	TCC	CGA	CTG	TTG	GAG	AAG	GAA	AAC	CGA	GAA	2688
	Asn	Asn	Glu	Glu	Glu	Lys	Ser	Arg	Leu	Leu	Glu	Lys	Glu	Asn	Arg	Glu	
						885					890				895		
40	CTG	GAA	AAG	ATC	ATC	GCT	GAG	AAA	GAG	GAG	CGC	GTC	TCT	GAA	CTG	CGC	2736
	Leu	Glu	Lys	Ile	Ile	Ala	Glu	Lys	Glu	Glu	Arg	Val	Ser	Glu	Leu	Arg	
				900					905					910			



CAT CAG CTC CAG TCT CGG CAG CAA CTC CGC TCA CGG CGC CAC CCC CCA 2784  
 His Gln Leu Gln Ser Arg Gln Gln Leu Arg Ser Arg Arg His Pro Pro  
 915 920 925

5 ACA CCC CCA GAT CCC TCT GGG GGC CTT CCC AGG GGA CCC TCT GAG CCC 2832  
 Thr Pro Pro Asp Pro Ser Gly Gly Leu Pro Arg Gly Pro Ser Glu Pro  
 930 935 940

CCT GAC CGG CTT AGC TGT GAT GGG AGT CGA GTA CAT TTG CTT TAC AAG 2880  
 10 Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg Val His Leu Leu Tyr Lys  
 945 950 955 960

TGA 2883  
 \*

15

## (2) INFORMATION FOR SEQ ID NO: 45:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 960 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

Met Leu Leu Leu Leu Leu Val Pro Leu Phe Leu Arg Pro Leu Gly Ala  
 1 5 10 15

30 Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile Ile  
 20 25 30

His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg Asp  
 35 35 40 45

Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu Tyr  
 50 55 60

40 Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys Cys  
 65 70 75 80

Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys Val

	85	90	95
	Arg Ile Cys Ser Lys Ser Tyr Leu Thr Leu Glu Asn Gly Lys Val Phe		
	100	105	110
5	Leu Thr Gly Gly Asp Leu Pro Ala Leu Asp Gly Ala Arg Val Glu Phe		
	115	120	125
	Arg Cys Asp Pro Asp Phe His Leu Val Gly Ser Ser Arg Ser Val Cys		
10	130	135	140
	Ser Gln Gly Gln Trp Ser Thr Pro Lys Pro His Cys Gln Val Asn Arg		
	145	150	155
15	Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe Pro		
	165	170	175
	Met Ser Gly Gly Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val Glu		
	180	185	190
20	Met Ala Leu Glu Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp Tyr		
	195	200	205
	Glu Leu Lys Leu Ile His His Asp Ser Lys Cys Asp Pro Gly Gln Ala		
25	210	215	220
	Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile Ile		
	225	230	235
30	Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala		
	245	250	255
	Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala		
	260	265	270
35	Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro Ser		
	275	280	285
	Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp Gly		
40	290	295	300
	Trp Lys Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr Ser		
	305	310	315
			320

Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu Ile  
 325 330 335

5 Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys Asn  
 340 345 350

Leu Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu Thr  
 355 360 365

10 Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly  
 370 375 380

Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe  
 15 385 390 395 400

Lys Thr Tyr Asp Pro Ser Ile Asn Cys Thr Val Glu Glu Met Thr Glu  
 405 410 415

20 Ala Val Glu Gly His Ile Thr Thr Glu Ile Val Met Leu Asn Pro Ala  
 420 425 430

Asn Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu Lys  
 435 440 445

25 Leu Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln  
 450 455 460

Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Leu  
 30 465 470 475 480

Asn Lys Thr Ser Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu Asp  
 485 490 495

35 Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala Met  
 500 505 510

Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val Val Phe Asp Ala  
 515 520 525

40 Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly Gly  
 530 535 540

Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu Ser  
 545 550 555 560

Trp Ser Lys Thr Asp Lys Trp Ile Gly Gly Ser Pro Pro Ala Asp Gln  
 5 565 570 575

Thr Leu Val Ile Lys Thr Phe Arg Phe Leu Ser Gln Lys Leu Phe Ile  
 580 585 590

10 Ser Val Ser Val Leu Ser Ser Leu Gly Ile Val Leu Ala Val Val Cys  
 595 600 605

Leu Ser Phe Asn Ile Tyr Asn Ser His Val Arg Tyr Ile Gln Asn Ser  
 610 615 620

15 Gln Pro Asn Leu Asn Asn Leu Thr Ala Val Gly Cys Ser Leu Ala Leu  
 625 630 635 640

Ala Ala Val Phe Pro Leu Gly Leu Asp Gly Tyr His Ile Gly Arg Ser  
 20 645 650 655

Gln Phe Pro Phe Val Cys Gln Ala Arg Leu Trp Leu Leu Gly Leu Gly  
 660 665 670

25 Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr Lys Ile Trp Trp Val His  
 675 680 685

Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp Arg Lys Thr Leu  
 690 695 700

30 Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly Leu Leu Val Gly Met Asp  
 705 710 715 720

Val Leu Thr Leu Ala Ile Trp Gln Ile Val Asp Pro Leu His Arg Thr  
 35 725 730 735

Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys Glu Asp Ile Asp Val Ser  
 740 745 750

40 Ile Leu Pro Gln Leu Glu His Cys Ser Ser Lys Lys Met Asn Thr Trp  
 755 760 765

Leu Gly Ile Phe Tyr Gly Tyr Lys Gly Leu Leu Leu Leu Gly Ile

	770	775	780	
	Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser Thr Glu Lys Ile Asn Asp			
	785	790	795	800
5	His Arg Ala Val Gly Met Ala Ile Tyr Asn Val Ala Val Leu Cys Leu			
		805	810	815
	Ile Thr Ala Pro Val Thr Met Ile Leu Ser Ser Gln Gln Asp Ala Ala			
10		820	825	830
	Phe Ala Phe Ala Ser Leu Ala Ile Val Phe Ser Ser Tyr Ile Thr Leu			
		835	840	845
15	Val Val Leu Phe Val Pro Lys Met Arg Arg Leu Ile Thr Arg Gly Glu			
		850	855	860
	Trp Gln Ser Glu Thr Gln Asp Thr Met Lys Thr Gly Ser Ser Thr Asn			
	865	870	875	880
20	Asn Asn Glu Glu Glu Lys Ser Arg Leu Leu Glu Lys Glu Asn Arg Glu			
		885	890	895
	Leu Glu Lys Ile Ile Ala Glu Lys Glu Glu Arg Val Ser Glu Leu Arg			
25		900	905	910
	His Gln Leu Gln Ser Arg Gln Gln Leu Arg Ser Arg Arg His Pro Pro			
		915	920	925
30	Thr Pro Pro Asp Pro Ser Gly Gly Leu Pro Arg Gly Pro Ser Glu Pro			
		930	935	940
	Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg Val His Leu Leu Tyr Lys			
	945	950	955	960

35

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 2538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

5

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Rattus norvegicus

10

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..2532

15

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Kaupmann, K

Huggel, K

Heid, J

Flor, P

20

Bischoff, M

Mickel, S

McMaster, G

Angst, C

Bittiger, H

25

Froestl, W

(B) TITLE: Expression cloning of GABA-B receptors

uncovers similarity to metabotropic glutamate  
receptors

(C) JOURNAL: Nature

30

(D) VOLUME: 386

(F) PAGES: 239-246

(G) DATE: 20 March-1997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

35

ATG GGC CCG GGG GGA CCC TGT ACC CCA GTG GGG TGG CCG CTG CCT CTT

48

Met Gly Pro Gly Gly Pro Cys Thr Pro Val Gly Trp Pro Leu Pro Leu

1

5

10

15

40

CTG CTG GTG ATG GCG GCT GGG GTG GCT CCG GTG TGG GCC TCT CAC TCC

96,

Leu Leu Val Met Ala Ala Gly Val Ala Pro Val Trp Ala Ser His Ser

20

25

30

	CCT CAT CTC CCG CGG CCT CAC CCG AGG GTC CCC CCG CAC CCC TCC TCA	144
	Pro His Leu Pro Arg Pro His Pro Arg Val Pro Pro His Pro Ser Ser	
	35 40 45	
5	GAA CGG CGT GCA GTA TAC ATC GGG GCG CTG TTT CCC ATG AGC GGG GGC	192
	Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe Pro Met Ser Gly Gly	
	50 55 60	
	TGG CCG GGG GGC CAG GCC TGC CAG CCC GCG GTG GAG ATG GCG CTG GAG	240
10	Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val Glu Met Ala Leu Glu	
	65 70 75 80	
	GAC GTT AAC AGC CGC AGA GAC ATC CTG CCG GAC TAC GAG CTC AAG CTT	288
	Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp Tyr Glu Leu Lys Leu	
15	85 90 95	
	ATC CAC CAC GAC AGC AAG TGT GAC CCA GGG CAA GCC ACC AAG TAC TTG	336
	Ile His His Asp Ser Lys Cys Asp Pro Gly Gln Ala Thr Lys Tyr Leu	
	100 105 110	
20	TAC GAA CTA CTC TAC AAT GAC CCC ATC AAG ATC ATT CTC ATG CCT GGC	384
	Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile Ile Leu Met Pro Gly	
	115 120 125	
25	TGT AGT TCT GTC TCC ACA CTT GTA GCT GAG GCT GCC CGG ATG TGG AAC	432
	Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala Arg Met Trp Asn	
	130 135 140	
	CTT ATT GTG CTC TCA TAT GGC TCC AGT TCA CCA GCC TTG TCA AAC CGA	480
30	Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala Leu Ser Asn Arg	
	145 150 155 160	
	CAG CGG TTT CCC ACG TTC TTC CGG ACG CAT CCA TCC GCC ACA CTC CAC	528
	Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro Ser Ala Thr Leu His	
35	165 170 175	
	AAT CCC ACC CGG GTG AAA CTC TTC GAA AAG TGG GGC TGG AAG AAG ATC	576
	Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp Gly Trp Lys Lys Ile	
	180 185 190	
40	GCT ACC ATC CAA CAG ACC ACC GAG GTC TTC ACC TCA ACG CTG GAT GAC	624
	Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr Ser Thr Leu Asp Asp	
	195 200 205	

	CTG GAG GAG CGA GTG AAA GAG GCT GGG ATC GAG ATC ACT TTC CGA CAG	672
	Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu Ile Thr Phe Arg Gln	
	210 215 220	
5	AGT TTC TTC TCG GAT CCA GCT GTG CCT GTT AAA AAC CTG AAG CGT CAA	720
	Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys Asn Leu Lys Arg Gln	
	225 230 235 240	
10	GAT GCT CGA ATC ATC GTG GGA CTT TTC TAT GAG ACG GAA GCC CGG AAA	768
	Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu Thr Glu Ala Arg Lys	
	245 250 255	
	GTT TTT TGT GAG GTC TAT AAG GAA AGG CTC TTT GGG AAG AAG TAC GTC	816
15	Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly Lys Lys Tyr Val	
	260 265 270	
	TGG TTC CTC ATC GGG TGG TAT GCT GAC AAC TGG TTC AAG ACC TAT GAC	864
	Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe Lys Thr Tyr Asp	
20	275 280 285	
	CCG TCA ATC AAT TGT ACA GTG GAA GAA ATG ACC GAG GCG GTG GAG GGC	912
	Pro Ser Ile Asn Cys Thr Val Glu Glu Met Thr Glu Ala Val Glu Gly	
	290 295 300	
25	CAC ATC ACC ACG GAG ATT GTC ATG CTG AAC CCT GCC AAC ACC CGA AGC	960
	His Ile Thr Thr Glu Ile Val Met Leu Asn Pro Ala Asn Thr Arg Ser	
	305 310 315 320	
30	ATT TCC AAC ATG ACG TCA CAG GAA TTT GTG GAG AAA CTA ACC AAG CGG	1008
	Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu Lys Leu Thr Lys Arg	
	325 330 335	
	CTG AAA AGA CAC CCC GAG GAG ACT GGA GGC TTC CAG GAG GCA CCA CTG	1056
35	Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln Glu Ala Pro Leu	
	340 345 350	
	GCC TAT GAT GCT ATC TGG GCC TTG GCT TTG GCC TTG AAC AAG ACG TCT	1104
	Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Leu Asn Lys Thr Ser	
40	355 360 365	
	GGA GGA GGT GGT CGT TCC GGC GTG CGC CTG GAG GAC TTT AAC TAC AAC	1152
	Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu Asp Phe Asn Tyr Asn	



	370	375	380	
	AAC CAG ACC ATT ACA GAC CAG ATC TAC CGG GCC ATG AAC TCC TCC TCC			1200
	Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala Met Asn Ser Ser Ser			
5	385	390	395	400
	TTT GAG GGC GTT TCT GGC CAT GTG GTC TTT GAT GCC AGC GGC TCC CGG			1248
	Phe Glu Gly Val Ser Gly His Val Val Phe Asp Ala Ser Gly Ser Arg			
	405	410	415	
10	ATG GCA TGG ACA CTT ATC GAG CAG CTA CAG GGC GGC AGC TAC AAG AAG			1296
	Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly Gly Ser Tyr Lys Lys			
	420	425	430	
15	ATC GGC TAC TAC GAC AGC ACC AAG GAT GAT CTT TCC TGG TCC AAA ACG			1344
	Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu Ser Trp Ser Lys Thr			
	435	440	445	
	GAC AAG TGG ATT GGA GGC TCT CCC CCA GCT GAC CAG ACC TTG GTC ATC			1392
20	Asp Lys Trp Ile Gly Gly Ser Pro Pro Ala Asp Gln Thr Leu Val Ile			
	450	455	460	
	AAG ACA TTC CGT TTC CTG TCT CAG AAA CTC TTT ATC TCC GTC TCA GTT			1440
	Lys Thr Phe Arg Phe Leu Ser Gln Lys Leu Phe Ile Ser Val Ser Val			
25	465	470	475	480
	CTC TCC AGC CTG GGC ATT GTT CTT GCT GTT GTC TGT CTG TCC TTT AAC			1488
	Leu Ser Ser Leu Gly Ile Val Leu Ala Val Val Cys Leu Ser Phe Asn			
	485	490	495	
30	ATC TAC AAC TCC CAC GTT CGT TAT ATC CAG AAC TCC CAG CCC AAC CTG			1536
	Ile Tyr Asn Ser His Val Arg Tyr Ile Gln Asn Ser Gln Pro Asn Leu			
	500	505	510	
35	AAC AAT CTG ACT GCT GTG GGC TGC TCA CTG GCA CTG GCT GCT GTC TTC			1584
	Asn Asn Leu Thr Ala Val Gly Cys Ser Leu Ala Leu Ala Ala Val Phe			
	515	520	525	
	CCT CTC GGG CTG GAT GGT TAC CAC ATA GGG AGA AGC CAG TTC CCG TTT			1632
40	Pro Leu Gly Leu Asp Gly Tyr His Ile Gly Arg Ser Gln Phe Pro Phe			
	530	535	540	
	GTC TGC CAG GCC CGC CTT TGG CTC TTG GGC TTG GGC TTT AGT CTG GGC			1680

	Val	Cys	Gln	Ala	Arg	Leu	Trp	Leu	Leu	Gly	Leu	Gly	Phe	Ser	Leu	Gly	
	545					550					555					560	
	TAT	GGC	TCT	ATG	TTC	ACC	AAG	ATC	TGG	TGG	GTC	CAC	ACA	GTC	TTC	ACG	1728
5	Tyr	Gly	Ser	Met	Phe	Thr	Lys	Ile	Trp	Trp	Val	His	Thr	Val	Phe	Thr	
					565				570					575			
	AAG	AAG	GAG	GAG	AAG	AAG	GAG	TGG	AGG	AAG	ACC	CTA	GAG	CCC	TGG	AAA	1776
10	Lys	Lys	Glu	Glu	Lys	Lys	Glu	Trp	Arg	Lys	Thr	Leu	Glu	Pro	Trp	Lys	
					580				585					590			
	CTC	TAT	GCC	ACT	GTG	GGC	CTG	CTG	GTG	GGC	ATG	GAT	GTC	CTG	ACT	CTT	1824
	Leu	Tyr	Ala	Thr	Val	Gly	Leu	Leu	Val	Gly	Met	Asp	Val	Leu	Thr	Leu	
					595				600					605			
15	GCC	ATC	TGG	CAG	ATT	GTG	GAC	CCC	TTG	CAC	CGA	ACC	ATT	GAG	ACT	TTT	1872
	Ala	Ile	Trp	Gln	Ile	Val	Asp	Pro	Leu	His	Arg	Thr	Ile	Glu	Thr	Phe	
					610				615					620			
20	GCC	AAG	GAG	GAA	CCA	AAG	GAA	GAC	ATC	GAT	GTC	TCC	ATT	CTG	CCC	CAG	1920
	Ala	Lys	Glu	Glu	Pro	Lys	Glu	Asp	Ile	Asp	Val	Ser	Ile	Leu	Pro	Gln	
					625				630					635		640	
	TTG	GAG	CAC	TGC	AGC	TCC	AAG	AAG	ATG	AAT	ACG	TGG	CTT	GGC	ATT	TTC	1968
25	Leu	Glu	His	Cys	Ser	Ser	Lys	Lys	Met	Asn	Thr	Trp	Leu	Gly	Ile	Phe	
					645				650					655			
	TAT	GGT	TAC	AAG	GGG	CTG	CTG	CTG	CTG	CTG	GGA	ATC	TTT	CTT	GCT	TAC	2016
30	Tyr	Gly	Tyr	Lys	Gly	Leu	Leu	Leu	Leu	Leu	Gly	Ile	Phe	Leu	Ala	Tyr	
					660				665					670			
	GAA	ACC	AAG	AGC	GTG	TCC	ACT	GAA	AAG	ATC	AAT	GAC	CAC	AGG	GCC	GTG	2064
	Glu	Thr	Lys	Ser	Val	Ser	Thr	Glu	Lys	Ile	Asn	Asp	His	Arg	Ala	Val	
					675				680					685			
35	GGC	ATG	GCT	ATC	TAC	AAT	GTC	GCG	GTC	CTG	TGT	CTC	ATC	ACT	GCT	CCT	2112
	Gly	Met	Ala	Ile	Tyr	Asn	Val	Ala	Val	Leu	Cys	Leu	Ile	Thr	Ala	Pro	
					690				695					700			
40	GTG	ACC	ATG	ATC	CTT	TCC	AGT	CAG	CAG	GAC	GCA	GCC	TTT	GCC	TTT	GCC	2160
	Val	Thr	Met	Ile	Leu	Ser	Ser	Gln	Gln	Asp	Ala	Ala	Phe	Ala	Phe	Ala	
					705				710					715		720	

	TCT CTG GCC ATC GTG TTC TCT TCC TAC ATC ACT CTG GTT GTG CTC TTT	2208
	Ser Leu Ala Ile Val Phe Ser Ser Tyr Ile Thr Leu Val Val Leu Phe	
	725 730 735	
5	GTG CCC AAG ATG CGC AGG CTG ATC ACC CGA GGG GAA TGG CAG TCT GAA	2256
	Val Pro Lys Met Arg Arg Leu Ile Thr Arg Gly Glu Trp Gln Ser Glu	
	740 745 750	
	ACG CAG GAC ACC ATG AAA ACA GGA TCA TCC ACC AAC AAC AAC GAG GAA	2304
10	Thr Gln Asp Thr Met Lys Thr Gly Ser Ser Thr Asn Asn Asn Glu Glu	
	755 760 765	
	GAG AAG TCC CGA CTG TTG GAG AAG GAA AAC CGA GAA CTG GAA AAG ATC	2352
	Glu Lys Ser Arg Leu Leu Glu Lys Glu Asn Arg Glu Leu Glu Lys Ile	
15	770 775 780	
	ATC GCT GAG AAA GAG GAG CGC GTC TCT GAA CTG CGC CAT CAG CTC CAG	2400
	Ile Ala Glu Lys Glu Glu Arg Val Ser Glu Leu Arg His Gln Leu Gln	
	785 790 795 800	
20	TCT CGG CAG CAA CTC CGC TCA CGG CGC CAC CCC CCA ACA CCC CCA GAT	2448
	Ser Arg Gln Gln Leu Arg Ser Arg Arg His Pro Pro Thr Pro Pro Asp	
	805 810 815	
25	CCC TCT GGG GGC CTT CCC AGG GGA CCC TCT GAG CCC CCT GAC CGG CTT	2496
	Pro Ser Gly Gly Leu Pro Arg Gly Pro Ser Glu Pro Pro Asp Arg Leu	
	820 825 830	
	AGC TGT GAT GGG AGT CGA GTA CAT TTG CTT TAC AAG TGA	2535
30	Ser Cys Asp Gly Ser Arg Val His Leu Leu Tyr Lys *	
	835 840	

## (2) INFORMATION FOR SEQ ID NO: 47:

35

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 844 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

Met Gly Pro Gly Gly Pro Cys Thr Pro Val Gly Trp Pro Leu Pro Leu  
 1 5 10 15  
 5 Leu Leu Val Met Ala Ala Gly Val Ala Pro Val Trp Ala Ser His Ser  
 20 25 30  
 Pro His Leu Pro Arg Pro His Pro Arg Val Pro Pro His Pro Ser Ser  
 35 40 45  
 10 Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe Pro Met Ser Gly Gly  
 50 55 60  
 Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val Glu Met Ala Leu Glu  
 15 65 70 75 80  
 Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp Tyr Glu Leu Lys Leu  
 85 90 95  
 20 Ile His His Asp Ser Lys Cys Asp Pro Gly Gln Ala Thr Lys Tyr Leu  
 100 105 110  
 Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile Ile Leu Met Pro Gly  
 115 120 125  
 25 Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala Arg Met Trp Asn  
 130 135 140  
 Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala Leu Ser Asn Arg  
 30 145 150 155 160  
 Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro Ser Ala Thr Leu His  
 165 170 175  
 35 Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp Gly Trp Lys Lys Ile  
 180 185 190  
 Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr Ser Thr Leu Asp Asp  
 195 200 205  
 40 Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu Ile Thr Phe Arg Gln  
 210 215 220

Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys Asn Leu Lys Arg Gln  
 225 230 235 240

Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu Thr Glu Ala Arg Lys  
 5 245 250 255

Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly Lys Lys Tyr Val  
 260 265 270

10 Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe Lys Thr Tyr Asp  
 275 280 285

Pro Ser Ile Asn Cys Thr Val Glu Glu Met Thr Glu Ala Val Glu Gly  
 290 295 300

15 His Ile Thr Thr Glu Ile Val Met Leu Asn Pro Ala Asn Thr Arg Ser  
 305 310 315 320

Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu Lys Leu Thr Lys Arg  
 20 325 330 335

Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln Glu Ala Pro Leu  
 340 345 350

25 Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Leu Asn Lys Thr Ser  
 355 360 365

Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu Asp Phe Asn Tyr Asn  
 370 375 380

30 Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala Met Asn Ser Ser Ser  
 385 390 395 400

Phe Glu Gly Val Ser Gly His Val Val Phe Asp Ala Ser Gly Ser Arg  
 35 405 410 415

Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly Gly Ser Tyr Lys Lys  
 420 425 430

40 Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu Ser Trp Ser Lys Thr  
 435 440 445

Asp Lys Trp Ile Gly Gly Ser Pro Pro Ala Asp Gln Thr Leu Val Ile

	450		455		460	
	Lys Thr Phe Arg Phe Leu Ser Gln Lys Leu Phe Ile Ser Val Ser Val					
	465		470		475	480
5	Leu Ser Ser Leu Gly Ile Val Leu Ala Val Val Cys Leu Ser Phe Asn					
		485		490		495
	Ile Tyr Asn Ser His Val Arg Tyr Ile Gln Asn Ser Gln Pro Asn Leu					
10		500		505		510
	Asn Asn Leu Thr Ala Val Gly Cys Ser Leu Ala Leu Ala Ala Val Phe					
		515		520		525
15	Pro Leu Gly Leu Asp Gly Tyr His Ile Gly Arg Ser Gln Phe Pro Phe					
		530		535		540
	Val Cys Gln Ala Arg Leu Trp Leu Leu Gly Leu Gly Phe Ser Leu Gly					
		545		550		555
20	Tyr Gly Ser Met Phe Thr Lys Ile Trp Trp Val His Thr Val Phe Thr					
		565		570		575
	Lys Lys Glu Glu Lys Lys Glu Trp Arg Lys Thr Leu Glu Pro Trp Lys					
25		580		585		590
	Leu Tyr Ala Thr Val Gly Leu Leu Val Gly Met Asp Val Leu Thr Leu					
		595		600		605
30	Ala Ile Trp Gln Ile Val Asp Pro Leu His Arg Thr Ile Glu Thr Phe					
		610		615		620
	Ala Lys Glu Glu Pro Lys Glu Asp Ile Asp Val Ser Ile Leu Pro Gln					
		625		630		635
35	Leu Glu His Cys Ser Ser Lys Lys Met Asn Thr Trp Leu Gly Ile Phe					
		645		650		655
	Tyr Gly Tyr Lys Gly Leu Leu Leu Leu Leu Gly Ile Phe Leu Ala Tyr					
40		660		665		670
	Glu Thr Lys Ser Val Ser Thr Glu Lys Ile Asn Asp His Arg Ala Val					
		675		680		685

Gly Met Ala Ile Tyr Asn Val Ala Val Leu Cys Leu Ile Thr Ala Pro  
 690 695 700  
 5 Val Thr Met Ile Leu Ser Ser Gln Gln Asp Ala Ala Phe Ala Phe Ala  
 705 710 715 720  
 Ser Leu Ala Ile Val Phe Ser Ser Tyr Ile Thr Leu Val Val Leu Phe  
 725 730 735  
 10 Val Pro Lys Met Arg Arg Leu Ile Thr Arg Gly Glu Trp Gln Ser Glu  
 740 745 750  
 Thr Gln Asp Thr Met Lys Thr Gly Ser Ser Thr Asn Asn Asn Glu Glu  
 15 755 760 765  
 Glu Lys Ser Arg Leu Leu Glu Lys Glu Asn Arg Glu Leu Glu Lys Ile  
 770 775 780  
 20 Ile Ala Glu Lys Glu Glu Arg Val Ser Glu Leu Arg His Gln Leu Gln  
 785 790 795 800  
 Ser Arg Gln Gln Leu Arg Ser Arg Arg His Pro Pro Thr Pro Pro Asp  
 805 810 815  
 25 Pro Ser Gly Gly Leu Pro Arg Gly Pro Ser Glu Pro Pro Asp Arg Leu  
 820 825 830  
 Ser Cys Asp Gly Ser Arg Val His Leu Leu Tyr Lys  
 30 835 840

## (2). INFORMATION FOR SEQ ID NO: 48:

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2886 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 40  
 (ii) MOLECULE TYPE: cDNA to mRNA  
 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

5 (A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..2886

10.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

	ATG TTG CTG CTG CTG CTA CTG GCG CCA CTC TTC CTC CGC CCC CCG GGC	48
	Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly	
15	1 5 10 15	
	GCG GGC GGG GCG CAG ACC CCC AAC GCC ACC TCA GAA GGT TGC CAG ATC	96
	Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile	
	20 25 30	
20	ATA CAC CCG CCC TGG GAA GGG GGC ATC AGG TAC CGG GGC CTG ACT CGG	144
	Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg	
	35 40 45	
25	GAC CAG GTG AAG GCT ATC AAC TTC CTG CCA GTG GAC TAT GAG ATT GAG	192
	Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu	
	50 55 60	
	TAT GTG TGC CGG GGG GAG CGC GAG GTG GTG GGG CCC AAG GTC CGC AAG	240
30	Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys	
	65 70 75 80	
	TGC CTG GCC AAC GGC TCC TGG ACA GAT ATG GAC ACA CCC AGC CGC TGT	288
	Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys	
35	85 90 95	
	GTC CGA ATC TGC TCC AAG TCT TAT TTG ACC CTG GAA AAT GGG AAG GTT	336
	Val Arg Ile Cys Ser Lys Ser Tyr Leu Thr Leu Glu Asn Gly Lys Val	
	100 105 110	
40	TTC CTG ACG GGT GGG GAC CTC CCA GCT CTG GAC GGA GCC CGG GTG GAT	384
	Phe Leu Thr Gly Gly Asp Leu Pro Ala Leu Asp Gly Ala Arg Val Asp	
	115 120 125	



	TTC CGG TGT GAC CCC GAC TTC CAT CTG GTG GGC AGC TCC CGG AGC ATC	432
	Phe Arg Cys Asp Pro Asp Phe His Leu Val Gly Ser Ser Arg Ser Ile	
	130 135 140	
5	TGT AGT CAG GGC CAG TGG AGC ACC CCC AAG CCC CAC TGC CAG GTG AAT	480
	Cys Ser Gln Gly Gln Trp Ser Thr Pro Lys Pro His Cys Gln Val Asn	
	145 150 155 160	
10	CGA ACG CCA CAC TCA GAA CGG CGC GCA GTG TAC ATC GGG GCA CTG TTT	528
	Arg Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe	
	165 170 175	
	CCC ATG AGC GGG GGC TGG CCA GGG GGC CAG GCC TGC CAG CCC GCG GTG	576
15	Pro Met Ser Gly Gly Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val	
	180 185 190	
	GAG ATG GCG CTG GAG GAC GTG AAT AGC CGC AGG GAC ATC CTG CCG GAC	624
	Glu Met Ala Leu Glu Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp	
20	195 200 205	
	TAT GAG CTC AAG CTC ATC CAC CAC GAC AGC AAG TGT GAT CCA GGC CAA	672
	Tyr Glu Leu Lys Leu Ile His His Asp Ser Lys Cys Asp Pro Gly Gln	
	210 215 220	
25	GCC ACC AAG TAC CTA TAT GAG CTG CTC TAC AAC GAC CCT ATC AAG ATC	720
	Ala Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile	
	225 230 235 240	
30	ATC CTT ATG CCT GGC TGC AGC TCT GTC TCC ACG CTG GTG GCT GAG GCT	768
	Ile Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala	
	245 250 255	
	GCT AGG ATG TGG AAC CTC ATT GTG CTT TCC TAT GGC TCC AGC TCA CCA	816
35	Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro	
	260 265 270	
	GCC CTG TCA AAC CGG CAG CGT TTC CCC ACT TTC TTC CGA ACG CAC CCA	864
	Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro	
40	275 280 285	
	TCA GCC ACA CTC CAC AAC CCT ACC CGC GTG AAA CTC TTT GAA AAG TGG	912
	Ser Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp	

40

	Gln	Glu	Ala	Pro	Leu	Ala	Tyr	Asp	Ala	Ile	Trp	Ala	Leu	Ala	Leu	Ala	
	465					470					475					480	
	CTG	AAC	AAG	ACA	TCT	GGA	GGA	GGC	GGC	CGT	TCT	GGT	GTG	CGC	CTG	GAG	1488
5	Leu	Asn	Lys	Thr	Ser	Gly	Gly	Gly	Gly	Arg	Ser	Gly	Val	Arg	Leu	Glu	
						485				490					495		
	GAC	TTC	AAC	TAC	AAC	AAC	CAG	ACC	ATT	ACC	GAC	CAA	ATC	TAC	CGG	GCA	1536
10	Asp	Phe	Asn	Tyr	Asn	Asn	Gln	Thr	Ile	Thr	Asp	Gln	Ile	Tyr	Arg	Ala	
				500					505					510			
	ATG	AAC	TCT	TCG	TCC	TTT	GAG	GGT	GTC	TCT	GGC	CAT	GTG	GTG	TTT	GAT	1584
	Met	Asn	Ser	Ser	Ser	Phe	Glu	Gly	Val	Ser	Gly	His	Val	Val	Phe	Asp	
			515					520					525				
15																	
	GCC	AGC	GGC	TCT	CGG	ATG	GCA	TGG	ACG	CTT	ATC	GAG	CAG	CTT	CAG	GGT	1632
	Ala	Ser	Gly	Ser	Arg	Met	Ala	Trp	Thr	Leu	Ile	Glu	Gln	Leu	Gln	Gly	
			530					535					540				
20																	
	GGC	AGC	TAC	AAG	AAG	ATT	GGC	TAC	TAT	GAC	AGC	ACC	AAG	GAT	GAT	CTT	1680
	Gly	Ser	Tyr	Lys	Lys	Ile	Gly	Tyr	Tyr	Asp	Ser	Thr	Lys	Asp	Asp	Leu	
	545					550					555					560	
25																	
	TCC	TGG	TCC	AAA	ACA	GAT	AAA	TGG	ATT	GGA	GGG	TCC	CCC	CCA	GCT	GAC	1728
	Ser	Trp	Ser	Lys	Thr	Asp	Lys	Trp	Ile	Gly	Gly	Ser	Pro	Pro	Ala	Asp	
						565				570					575		
30																	
	CAG	ACC	CTG	GTC	ATC	AAG	ACA	TTC	CGC	TTC	CTG	TCA	CAG	AAA	CTC	TTT	1776
	Gln	Thr	Leu	Val	Ile	Lys	Thr	Phe	Arg	Phe	Leu	Ser	Gln	Lys	Leu	Phe	
				580						585					590		
35																	
	ATC	TCC	GTC	TCA	GTT	CTC	TCC	AGC	CTG	GGC	ATT	GTC	CTA	GCT	GTT	GTC	1824
	Ile	Ser	Val	Ser	Val	Leu	Ser	Ser	Leu	Gly	Ile	Val	Leu	Ala	Val	Val	
				595					600						605		
40																	
	TGT	CTG	TCC	TTT	AAC	ATC	TAC	AAC	TCA	CAT	GTC	CGT	TAT	ATC	CAG	AAC	1872
	Cys	Leu	Ser	Phe	Asn	Ile	Tyr	Asn	Ser	His	Val	Arg	Tyr	Ile	Gln	Asn	
				610					615						620		
40																	
	TCA	CAG	CCC	AAC	CTG	AAC	AAC	CTG	ACT	GCT	GTG	GGC	TGC	TCA	CTG	GCT	1920
	Ser	Gln	Pro	Asn	Leu	Asn	Asn	Leu	Thr	Ala	Val	Gly	Cys	Ser	Leu	Ala	
	625					630					635				640		

	TTA GCT GCT GTC TTC CCC CTG GGG CTC GAT GGT TAC CAC ATT GGG AGG	1968
	Leu Ala Ala Val Phe Pro Leu Gly Leu Asp Gly Tyr His Ile Gly Arg	
	645 650 655	
5	AAC CAG TTT CCT TTC GTC TGC CAG GCC CGC CTC TGG CTC CTG GGC CTG	2016
	Asn Gln Phe Pro Phe Val Cys Gln Ala Arg Leu Trp Leu Leu Gly Leu	
	660 665 670	
	GGC TTT AGT CTG GGC TAC GGT TCC ATG TTC ACC AAG ATT TGG TGG GTC	2064
10	Gly Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr Lys Ile Trp Trp Val	
	675 680 685	
	CAC ACG GTC TTC ACA AAG AAG GAA GAA AAG AAG GAG TGG AGG AAG ACT	2112
	His Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp Arg Lys Thr	
15	690 695 700	
	CTG GAA CCC TGG AAG CTG TAT GCC ACA GTG GGC CTG CTG GTG GGC ATG	2160
	Leu Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly Leu Leu Val Gly Met	
	705 710 715 720	
20	GAT GTC CTC ACT CTC GCC ATC TGG CAG ATC GTG GAC CCT CTG CAC CGG	2208
	Asp Val Leu Thr Leu Ala Ile Trp Gln Ile Val Asp Pro Leu His Arg	
	725 730 735	
25	ACC ATT GAG ACA TTT GCC AAG GAG GAA CCT AAG GAA GAT ATT GAC GTC	2256
	Thr Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys Glu Asp Ile Asp Val	
	740 745 750	
	TCT ATT CTG CCC CAG CTG GAG CAT TGC AGC TCC AGG AAG ATG AAT ACA	2304
30	Ser Ile Leu Pro Gln Leu Glu His Cys Ser Ser Arg Lys Met Asn Thr	
	755 760 765	
	TGG CTT GGC ATT TTC TAT GGT TAC AAG GGG CTG CTG CTG CTG CTG GGA	2352
	Trp Leu Gly Ile Phe Tyr Gly Tyr Lys Gly Leu Leu Leu Leu Leu Gly	
35	770 775 780	
	ATC TTC CTT GCT TAT GAG ACC AAG AGT GTG TCC ACT GAG AAG ATC AAT	2400
	Ile Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser Thr Glu Lys Ile Asn	
	785 790 795 800	
40	GAT CAC CGG GCT GTG GGC ATG GCT ATC TAC AAT GTG GCA GTC CTG TGC	2448
	Asp His Arg Ala Val Gly Met Ala Ile Tyr Asn Val Ala Val Leu Cys	
	805 810 815	

	CTC ATC ACT GCT CCT GTC ACC ATG ATT CTG TCC AGC CAG CAG GAT GCA	2496
	Leu Ile Thr Ala Pro Val Thr Met Ile Leu Ser Ser Gln Gln Asp Ala	
	820 825 830	
5	GCC TTT GCC TTT GCC TCT CTT GCC ATA GTT TTC TCC TCC TAT ATC ACT	2544
	Ala Phe Ala Phe Ala Ser Leu Ala Ile Val Phe Ser Ser Tyr Ile Thr	
	835 840 845	
10	CTT GTT GTG CTC TTT GTG CCC AAG ATG CGC AGG CTG ATC ACC CGA GGG	2592
	Leu Val Val Leu Phe Val Pro Lys Met Arg Arg Leu Ile Thr Arg Gly	
	850 855 860	
	GAA TGG CAG TCG GAG GCG CAG GAC ACC ATG AAG ACA GGG TCA TCG ACC	2640
15	Glu Trp Gln Ser Glu Ala Gln Asp Thr Met Lys Thr Gly Ser Ser Thr	
	865 870 875 880	
	AAC AAC AAC GAG GAG GAG AAG TCC CGG CTG TTG GAG AAG GAG AAC CGT	2688
	Asn Asn Asn Glu Glu Glu Lys Ser Arg Leu Leu Glu Lys Glu Asn Arg	
20	885 890 895	
	GAA CTG GAA AAG ATC ATT GCT GAG AAA GAG GAG CGT GTC TCT GAA CTG	2736
	Glu Leu Glu Lys Ile Ile Ala Glu Lys Glu Glu Arg Val Ser Glu Leu	
	900 905 910	
25	CGC CAT CAA CTC CAG TCT CGG CAG CAG CTC CGC TCC CGG CGC CAC CCA	2784
	Arg His Gln Leu Gln Ser Arg Gln Gln Leu Arg Ser Arg Arg His Pro	
	915 920 925	
30	CCG ACA CCC CCA GAA CCC TCT GGG GGC CTG CCC AGG GGA CCC CCT GAG	2832
	Pro Thr Pro Pro Glu Pro Ser Gly Gly Leu Pro Arg Gly Pro Pro Glu	
	930 935 940	
	CCC CCC GAC CGG CTT AGC TGT GAT GGG AGT CGA GTG CAT TTG CTT TAT	2880
35	Pro Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg Val His Leu Leu Tyr	
	945 950 955 960	
	AAG TGA	2886
	Lys *	

40

(2) INFORMATION FOR SEQ ID NO: 49:

H1865-1 WO SEQ

43

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 961 amino acids

(B) TYPE: amino acid

5 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

10

Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly  
 1 5 10 15

15

Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile  
 20 25 30

Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg  
 35 40 45

20

Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu  
 50 55 60

Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys  
 65 70 75 80

25

Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys  
 85 90 95

Val Arg Ile Cys Ser Lys Ser Tyr Leu Thr Leu Glu Asn Gly Lys Val  
 100 105 110

30

Phe Leu Thr Gly Gly Asp Leu Pro Ala Leu Asp Gly Ala Arg Val Asp  
 115 120 125

35

Phe Arg Cys Asp Pro Asp Phe His Leu Val Gly Ser Ser Arg Ser Ile  
 130 135 140

Cys Ser Gln Gly Gln Trp Ser Thr Pro Lys Pro His Cys Gln Val Asn  
 145 150 155 160

40

Arg Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe  
 165 170 175

Pro Met Ser Gly Gly Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val  
180 185 190

Glu Met Ala Leu Glu Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp  
5 195 200 205

Tyr Glu Leu Lys Leu Ile His His Asp Ser Lys Cys Asp Pro Gly Gln  
210 215 220

10 Ala Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile  
225 230 235 240

Ile Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala  
245 250 255

15 Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro  
260 265 270

Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro  
20 275 280 285

Ser Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp  
290 295 300

25 Gly Trp Lys Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr  
305 310 315 320

Ser Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu  
325 330 335

30 Ile Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys  
340 345 350

Asn Leu Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu  
35 355 360 365

Thr Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe  
370 375 380

40 Gly Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp  
385 390 395 400

Phe Lys Ile Tyr Asp Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr

	405	410	415
	Glu Ala Val Glu Gly His Ile Thr Thr Glu Ile Val Met Leu Asn Pro		
	420	425	430
5	Ala Asn Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu		
	435	440	445
	Lys Leu Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe		
10	450	455	460
	Gln Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala		
	465	470	475 480
15	Leu Asn Lys Thr Ser Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu		
	485	490	495
	Asp Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala		
	500	505	510
20	Met Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val Val Phe Asp		
	515	520	525
	Ala Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly		
25	530	535	540
	Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu		
	545	550	555 560
30	Ser Trp Ser Lys Thr Asp Lys Trp Ile Gly Gly Ser Pro Pro Ala Asp		
	565	570	575
	Gln Thr Leu Val Ile Lys Thr Phe Arg Phe Leu Ser Gln Lys Leu Phe		
	580	585	590
35	Ile Ser Val Ser Val Leu Ser Ser Leu Gly Ile Val Leu Ala Val Val		
	595	600	605
	Cys Leu Ser Phe Asn Ile Tyr Asn Ser His Val Arg Tyr Ile Gln Asn		
40	610	615	620
	Ser Gln Pro Asn Leu Asn Asn Leu Thr Ala Val Gly Cys Ser Leu Ala		
	625	630	635 640



Leu Ala Ala Val Phe Pro Leu Gly Leu Asp Gly Tyr His Ile Gly Arg  
645 650 655

5 Asn Gln Phe Pro Phe Val Cys Gln Ala Arg Leu Trp Leu Leu Gly Leu  
660 665 670

Gly Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr Lys Ile Trp Trp Val  
675 680 685

10 His Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp Arg Lys Thr  
690 695 700

Leu Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly Leu Leu Val Gly Met  
15 705 710 715 720

Asp Val Leu Thr Leu Ala Ile Trp Gln Ile Val Asp Pro Leu His Arg  
725 730 735

20 Thr Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys Glu Asp Ile Asp Val  
740 745 750

Ser Ile Leu Pro Gln Leu Glu His Cys Ser Ser Arg Lys Met Asn Thr  
755 760 765

25 Trp Leu Gly Ile Phe Tyr Gly Tyr Lys Gly Leu Leu Leu Leu Leu Gly  
770 775 780

Ile Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser Thr Glu Lys Ile Asn  
30 785 790 795 800

Asp His Arg Ala Val Gly Met Ala Ile Tyr Asn Val Ala Val Leu Cys  
805 810 815

35 Leu Ile Thr Ala Pro Val Thr Met Ile Leu Ser Ser Gln Gln Asp Ala  
820 825 830

Ala Phe Ala Phe Ala Ser Leu Ala Ile Val Phe Ser Ser Tyr Ile Thr  
835 840 845

40 Leu Val Val Leu Phe Val Pro Lys Met Arg Arg Leu Ile Thr Arg Gly  
850 855 860

Glu Trp Gln Ser Glu Ala Gln Asp Thr Met Lys Thr Gly Ser Ser Thr  
 865 870 875 880  
 Asn Asn Asn Glu Glu Glu Lys Ser Arg Leu Leu Glu Lys Glu Asn Arg  
 5 885 890 895  
 Glu Leu Glu Lys Ile Ile Ala Glu Lys Glu Glu Arg Val Ser Glu Leu  
 900 905 910  
 10 Arg His Gln Leu Gln Ser Arg Gln Gln Leu Arg Ser Arg Arg His Pro  
 915 920 925  
 Pro Thr Pro Pro Glu Pro Ser Gly Gly Leu Pro Arg Gly Pro Pro Glu  
 930 935 940  
 15 Pro Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg Val His Leu Leu Tyr  
 945 950 955 960  
 Lys  
 20

## (2) INFORMATION FOR SEQ ID NO: 50:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2535 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 30  
 (ii) MOLECULE TYPE: cDNA to rRNA  
 (iii) HYPOTHETICAL: NO  
 35 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens  
 40 (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..2535

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

5	1	5	10	15	48
	ATG GGG CCC GGG GCC CCT TTT GCC CGG GTG GGG TGG CCA CTG CCG CTT				
	Met Gly Pro Gly Ala Pro Phe Ala Arg Val Gly Trp Pro Leu Pro Leu				
10	20	25	30		
	CTG GTT GTG ATG GCG GCA GGG GTG GCT CCG GTG TGG GCC TCC CAC TCC				96
	Leu Val Val Met Ala Ala Gly Val Ala Pro Val Trp Ala Ser His Ser				
15	35	40	45		
	CCC CAT CTC CCG CGG CCT CAC TCG CGG GTC CCC CCG CAC CCC TCC TCA				144
	Pro His Leu Pro Arg Pro His Ser Arg Val Pro Pro His Pro Ser Ser				
20	50	55	60		
	GAA CGG CGC GCA GTG TAC ATC GGG GCA CTG TTT CCC ATG AGC GGG GGC				192
	Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe Pro Met Ser Gly Gly				
25	65	70	75	80	
	TGG CCA GGG GGC CAG GCC TGC CAG CCC GCG GTG GAG ATG GCG CTG GAG				240
	Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val Glu Met Ala Leu Glu				
30	85	90	95		
	GAC GTG AAT AGC CGC AGG GAC ATC CTG CCG GAC TAT GAG CTC AAG CTC				288
	Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp Tyr Glu Leu Lys Leu				
35	100	105	110		
	ATC CAC CAC GAC AGC AAG TGT GAT CCA GGC CAA GCC ACC AAG TAC CTA				336
	Ile His His Asp Ser Lys Cys Asp Pro Gly Gln Ala Thr Lys Tyr Leu				
40	115	120	125		
	TAT GAG CTG CTC TAC AAC GAC CCT ATC AAG ATC ATC CTT ATG CCT GGC				384
	Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile Ile Leu Met Pro Gly				
45	130	135	140		
	TGC AGC TCT GTC TCC ACG CTG GTG GCT GAG GCT GCT AGG ATG TGG AAC				432
	Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala Arg Met Trp Asn				
50	145	150	155	160	
	CTC ATT GTG CTT TCC TAT GGC TCC AGC TCA CCA GCC CTG TCA AAC CGG				480
	Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala Leu Ser Asn Arg				
55	165	170	175	180	
	CAG CGT TTC CCC ACT TTC TTC CGA ACG CAC CCA TCA GCC ACA CTC CAC				528

	Gln	Arg	Phe	Pro	Thr	Phe	Phe	Arg	Thr	His	Pro	Ser	Ala	Thr	Leu	His	
					165					170					175		
	AAC	CCT	ACC	CGC	GTG	AAA	CTC	TTT	GAA	AAG	TGG	GGC	TGG	AAG	AAG	ATT	576
5	Asn	Pro	Thr	Arg	Val	Lys	Leu	Phe	Glu	Lys	Trp	Gly	Trp	Lys	Lys	Ile	
					180					185					190		
	GCT	ACC	ATC	CAG	CAG	ACC	ACT	GAG	GTC	TTC	ACT	TCG	ACT	CTG	GAC	GAC	624
	Ala	Thr	Ile	Gln	Gln	Thr	Thr	Glu	Val	Phe	Thr	Ser	Thr	Leu	Asp	Asp	
10					195					200					205		
	CTG	GAG	GAA	CGA	GTG	AAG	GAG	GCT	GGA	ATT	GAG	ATT	ACT	TTC	CGC	CAG	672
	Leu	Glu	Glu	Arg	Val	Lys	Glu	Ala	Gly	Ile	Glu	Ile	Thr	Phe	Arg	Gln	
					210					215					220		
15																	
	AGT	TTC	TTC	TCA	GAT	CCA	GCT	GTG	CCC	GTC	AAA	AAC	CTG	AAG	CGC	CAG	720
	Ser	Phe	Phe	Ser	Asp	Pro	Ala	Val	Pro	Val	Lys	Asn	Leu	Lys	Arg	Gln	
					225					230					235		240
20																	
	GAT	GCC	CGA	ATC	ATC	GTG	GGA	CTT	TTC	TAT	GAG	ACT	GAA	GCC	CGG	AAA	768
	Asp	Ala	Arg	Ile	Ile	Val	Gly	Leu	Phe	Tyr	Glu	Thr	Glu	Ala	Arg	Lys	
						245				250					255		
	GTT	TTT	TGT	GAG	GTG	TAC	AAG	GAG	CGT	CTC	TTT	GGG	AAG	AAG	TAC	GTC	816
25	Val	Phe	Cys	Glu	Val	Tyr	Lys	Glu	Arg	Leu	Phe	Gly	Lys	Lys	Tyr	Val	
					260					265					270		
	TGG	TTC	CTC	ATT	GGG	TGG	TAT	GCT	GAC	AAT	TGG	TTC	AAG	ATC	TAC	GAC	864
	Trp	Phe	Leu	Ile	Gly	Trp	Tyr	Ala	Asp	Asn	Trp	Phe	Lys	Ile	Tyr	Asp	
30					275					280					285		
	CCT	TCT	ATC	AAC	TGC	ACA	GTG	GAT	GAG	ATG	ACT	GAG	GCG	GTG	GAG	GGC	912
	Pro	Ser	Ile	Asn	Cys	Thr	Val	Asp	Glu	Met	Thr	Glu	Ala	Val	Glu	Gly	
					290					295					300		
35																	
	CAC	ATC	ACA	ACT	GAG	ATT	GTC	ATG	CTG	AAT	CCT	GCC	AAT	ACC	CGC	AGC	960
	His	Ile	Thr	Thr	Glu	Ile	Val	Met	Leu	Asn	Pro	Ala	Asn	Thr	Arg	Ser	
					305					310					315		320
40																	
	ATT	TCC	AAC	ATG	ACA	TCC	CAG	GAA	TTT	GTG	GAG	AAA	CTA	ACC	AAG	CGA	1008
	Ile	Ser	Asn	Met	Thr	Ser	Gln	Glu	Phe	Val	Glu	Lys	Leu	Thr	Lys	Arg	
										325					330		335

	CTG AAA AGA CAC CCT GAG GAG ACA GGA GGC TTC CAG GAG GCA CCG CTG	1056
	Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln Glu Ala Pro Leu	
	340 345 350	
5	GCC TAT GAT GCC ATC TGG GCC TTG GCA CTG GCC CTG AAC AAG ACA TCT	1104
	Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Leu Asn Lys Thr Ser	
	355 360 365	
	GGA GGA GGC GGC CGT TCT GGT GTG CGC CTG GAG GAC TTC AAC TAC AAC	1152
10	Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu Asp Phe Asn Tyr Asn	
	370 375 380	
	AAC CAG ACC ATT ACC GAC CAA ATC TAC CGG GCA ATG AAC TCT TCG TCC	1200
	Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala Met Asn Ser Ser Ser	
15	385 390 395 400	
	TTT GAG GGT GTC TCT GGC CAT GTG GTG TTT GAT GCC AGC GGC TCT CGG	1248
	Phe Glu Gly Val Ser Gly His Val Val Phe Asp Ala Ser Gly Ser Arg	
	405 410 415	
20	ATG GCA TGG ACG CTT ATC GAG CAG CTT CAG GGT GGC AGC TAC AAG AAG	1296
	Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly Gly Ser Tyr Lys Lys	
	420 425 430	
25	ATT GGC TAC TAT GAC AGC ACC AAG GAT GAT CTT TCC TGG TCC AAA ACA	1344
	Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu Ser Trp Ser Lys Thr	
	435 440 445	
	GAT AAA TGG ATT GGA GGG TCC CCC CCA GCT GAC CAG ACC CTG GTC ATC	1392
30	Asp Lys Trp Ile Gly Gly Ser Pro Pro Ala Asp Gln Thr Leu Val Ile	
	450 455 460	
	AAG ACA TTC CGC TTC CTG TCA CAG AAA CTC TTT ATC TCC GTC TCA GTT	1440
	Lys Thr Phe Arg Phe Leu Ser Gln Lys Leu Phe Ile Ser Val Ser Val	
35	465 470 475 480	
	CTC TCC AGC CTG GGC ATT GTC CTA GCT GTT GTC TGT CTG TCC TTT AAC	1488
	Leu Ser Ser Leu Gly Ile Val Leu Ala Val Val Cys Leu Ser Phe Asn	
	485 490 495	
40	ATC TAC AAC TCA CAT GTC CGT TAT ATC CAG AAC TCA CAG CCC AAC CTG	1536
	Ile Tyr Asn Ser His Val Arg Tyr Ile Gln Asn Ser Gln Pro Asn Leu	
	500 505 510	

	AAC AAC CTG ACT GCT GTG GGC TGC TCA CTG GCT TTA GCT GCT GTC TTC	1584
	Asn Asn Leu Thr Ala Val Gly Cys Ser Leu Ala Leu Ala Ala Val Phe	
	515 520 525	
5	CCC CTG GGG CTC GAT GGT TAC CAC ATT GGG AGG AAC CAG TTT CCT TTC	1632
	Pro Leu Gly Leu Asp Gly Tyr His Ile Gly Arg Asn Gln Phe Pro Phe	
	530 535 540	
10	GTC TGC CAG GCC CGC CTC TGG CTC CTG GGC CTG GGC TTT AGT CTG GGC	1680
	Val Cys Gln Ala Arg Leu Trp Leu Leu Gly Leu Gly Phe Ser Leu Gly	
	545 550 555 560	
	TAC GGT TCC ATG TTC ACC AAG ATT TGG TGG GTC CAC ACG GTC TTC ACA	1728
15	Tyr Gly Ser Met Phe Thr Lys Ile Trp Trp Val His Thr Val Phe Thr	
	565 570 575	
	AAG AAG GAA GAA AAG AAG GAG TGG AGG AAG ACT CTG GAA CCC TGG AAG	1776
	Lys Lys Glu Glu Lys Lys Glu Trp Arg Lys Thr Leu Glu Pro Trp Lys	
20	580 585 590	
	CTG TAT GCC ACA GTG GGC CTG CTG GTG GGC ATG GAT GTC CTC ACT CTC	1824
	Leu Tyr Ala Thr Val Gly Leu Leu Val Gly Met Asp Val Leu Thr Leu	
	595 600 605	
25	GCC ATC TGG CAG ATC GTG GAC CCT CTG CAC CGG ACC ATT GAG ACA TTT	1872
	Ala Ile Trp Gln Ile Val Asp Pro Leu His Arg Thr Ile Glu Thr Phe	
	610 615 620	
30	GCC AAG GAG GAA CCT AAG GAA GAT ATT GAC GTC TCT ATT CTG CCC CAG	1920
	Ala Lys Glu Glu Pro Lys Glu Asp Ile Asp Val Ser Ile Leu Pro Gln	
	625 630 635 640	
	CTG GAG CAT TGC AGC TCC AGG AAG ATG AAT ACA TGG CTT GGC ATT TTC	1968
35	Leu Glu His Cys Ser Ser Arg Lys Met Asn Thr Trp Leu Gly Ile Phe	
	645 650 655	
	TAT GGT TAC AAG GGG CTG CTG CTG CTG CTG GGA ATC TTC CTT GCT TAT	2016
	Tyr Gly Tyr Lys Gly Leu Leu Leu Leu Leu Gly Ile Phe Leu Ala Tyr	
40	660 665 670	
	GAG ACC AAG AGT GTG TCC ACT GAG AAG ATC AAT GAT CAC CGG GCT GTG	2064
	Glu Thr Lys Ser Val Ser Thr Glu Lys Ile Asn Asp His Arg Ala Val	

	675	680	685	
	GGC ATG GCT ATC TAC AAT GTG GCA GTC CTG TGC CTC ATC ACT GCT CCT	2112		
	Gly Met Ala Ile Tyr Asn Val Ala Val Leu Cys Leu Ile Thr Ala Pro			
5	690	695	700	
	GTC ACC ATG ATT CTG TCC AGC CAG CAG GAT GCA GCC TTT GCC TTT GCC	2160		
	Val Thr Met Ile Leu Ser Ser Gln Gln Asp Ala Ala Phe Ala Phe Ala			
	705	710	715	720
10	TCT CTT GCC ATA GTT TTC TCC TCC TAT ATC ACT CTT GTT GTG CTC TTT	2208		
	Ser Leu Ala Ile Val Phe Ser Ser Tyr Ile Thr Leu Val Val Leu Phe			
	725	730	735	
15	GTG CCC AAG ATG CGC AGG CTG ATC ACC CGA GGG GAA TGG CAG TCG GAG	2256		
	Val Pro Lys Met Arg Arg Leu Ile Thr Arg Gly Glu Trp Gln Ser Glu			
	740	745	750	
	GCG CAG GAC ACC ATG AAG ACA GGG TCA TCG ACC AAC AAC AAC GAG GAG	2304		
20	Ala Gln Asp Thr Met Lys Thr Gly Ser Ser Thr Asn Asn Asn Glu Glu			
	755	760	765	
	GAG AAG TCC CGG CTG TTG GAG AAG GAG AAC CGT GAA CTG GAA AAG ATC	2352		
	Glu Lys Ser Arg Leu Leu Glu Lys Glu Asn Arg Glu Leu Glu Lys Ile			
25	770	775	780	
	ATT GCT GAG AAA GAG GAG CGT GTC TCT GAA CTG CGC CAT CAA CTC CAG	2400		
	Ile Ala Glu Lys Glu Glu Arg Val Ser Glu Leu Arg His Gln Leu Gln			
	785	790	795	800
30	TCT CGG CAG CAG CTC CGC TCC CGG CGC CAC CCA CCG ACA CCC CCA GAA	2448		
	Ser Arg Gln Gln Leu Arg Ser Arg Arg His Pro Pro Thr Pro Pro Glu			
	805	810	815	
35	CCC TCT GGG GGC CTG CCC AGG GGA CCC CCT GAG CCC CCC GAC CGG CTT	2496		
	Pro Ser Gly Gly Leu Pro Arg Gly Pro Pro Glu Pro Pro Asp Arg Leu			
	820	825	830	
	AGC TGT GAT GGG AGT CGA GTG CAT TTG CTT TAT AAG TGA	2535		
40	Ser Cys Asp Gly Ser Arg Val His Leu Leu Tyr Lys *			
	835	840		

## (2) INFORMATION FOR SEQ ID NO: 51:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 844 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Met Gly Pro Gly Ala Pro Phe Ala Arg Val Gly Trp Pro Leu Pro Leu  
 1 5 10 15  
 Leu Val Val Met Ala Ala Gly Val Ala Pro Val Trp Ala Ser His Ser  
 20 25 30  
 Pro His Leu Pro Arg Pro His Ser Arg Val Pro Pro His Pro Ser Ser  
 35 40 45  
 Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe Pro Met Ser Gly Gly  
 50 55 60  
 Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val Glu Met Ala Leu Glu  
 65 70 75 80  
 Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp Tyr Glu Leu Lys Leu  
 85 90 95  
 Ile His His Asp Ser Lys Cys Asp Pro Gly Gln Ala Thr Lys Tyr Leu  
 100 105 110  
 Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile Ile Leu Met Pro Gly  
 115 120 125  
 Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala Arg Met Trp Asn  
 130 135 140  
 Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala Leu Ser Asn Arg  
 145 150 155 160  
 Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro Ser Ala Thr Leu His  
 165 170 175



Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp Gly Trp Lys Lys Ile  
 180 185 190

5 Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr Ser Thr Leu Asp Asp  
 195 200 205

Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu Ile Thr Phe Arg Gln  
 210 215 220

10 Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys Asn Leu Lys Arg Gln  
 225 230 235 240

Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu Thr Glu Ala Arg Lys  
 15 245 250 255

Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly Lys Lys Tyr Val  
 260 265 270

20 Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe Lys Ile Tyr Asp  
 275 280 285

Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr Glu Ala Val Glu Gly  
 290 295 300

25 His Ile Thr Thr Glu Ile Val Met Leu Asn Pro Ala Asn Thr Arg Ser  
 305 310 315 320

Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu Lys Leu Thr Lys Arg  
 30 325 330 335

Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln Glu Ala Pro Leu  
 340 345 350

35 Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Leu Asn Lys Thr Ser  
 355 360 365

Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu Asp Phe Asn Tyr Asn  
 370 375 380

40 Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala Met Asn Ser Ser Ser  
 385 390 395 400

Phe Glu Gly Val Ser Gly His Val Val Phe Asp Ala Ser Gly Ser Arg  
 405 410 415  
 Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly Gly Ser Tyr Lys Lys  
 5 420 425 430  
 Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu Ser Trp Ser Lys Thr  
 435 440 445  
 10 Asp Lys Trp Ile Gly Gly Ser Pro Pro Ala Asp Gln Thr Leu Val Ile  
 450 455 460  
 Lys Thr Phe Arg Phe Leu Ser Gln Lys Leu Phe Ile Ser Val Ser Val  
 465 470 475 480  
 15 Leu Ser Ser Leu Gly Ile Val Leu Ala Val Val Cys Leu Ser Phe Asn  
 485 490 495  
 Ile Tyr Asn Ser His Val Arg Tyr Ile Gln Asn Ser Gln Pro Asn Leu  
 20 500 505 510  
 Asn Asn Leu Thr Ala Val Gly Cys Ser Leu Ala Leu Ala Ala Val Phe  
 515 520 525  
 25 Pro Leu Gly Leu Asp Gly Tyr His Ile Gly Arg Asn Gln Phe Pro Phe  
 530 535 540  
 Val Cys Gln Ala Arg Leu Trp Leu Leu Gly Leu Gly Phe Ser Leu Gly  
 545 550 555 560  
 30 Tyr Gly Ser Met Phe Thr Lys Ile Trp Trp Val His Thr Val Phe Thr  
 565 570 575  
 Lys Lys Glu Glu Lys Lys Glu Trp Arg Lys Thr Leu Glu Pro Trp Lys  
 35 580 585 590  
 Leu Tyr Ala Thr Val Gly Leu Leu Val Gly Met Asp Val Leu Thr Leu  
 595 600 605  
 40 Ala Ile Trp Gln Ile Val Asp Pro Leu His Arg Thr Ile Glu Thr Phe  
 610 615 620  
 Ala Lys Glu Glu Pro Lys Glu Asp Ile Asp Val Ser Ile Leu Pro Gln

625                                      630                                      635                                      640  
 Leu Glu His Cys Ser Ser Arg Lys Met Asn Thr Trp Leu Gly Ile Phe  
    645                                      650                                      655  
 5  
 Tyr Gly Tyr Lys Gly Leu Leu Leu Leu Leu Gly Ile Phe Leu Ala Tyr  
    660                                      665                                      670  
 Glu Thr Lys Ser Val Ser Thr Glu Lys Ile Asn Asp His Arg Ala Val  
 10                                      675                                      680                                      685  
 Gly Met Ala Ile Tyr Asn Val Ala Val Leu Cys Leu Ile Thr Ala Pro  
    690                                      695                                      700  
 15 Val Thr Met Ile Leu Ser Ser Gln Gln Asp Ala Ala Phe Ala Phe Ala  
    705                                      710                                      715                                      720  
 Ser Leu Ala Ile Val Phe Ser Ser Tyr Ile Thr Leu Val Val Leu Phe  
    725                                      730                                      735  
 20 Val Pro Lys Met Arg Arg Leu Ile Thr Arg Gly Glu Trp Gln Ser Glu  
    740                                      745                                      750  
 Ala Gln Asp Thr Met Lys Thr Gly Ser Ser Thr Asn Asn Asn Glu Glu  
 25                                      755                                      760                                      765  
 Glu Lys Ser Arg Leu Leu Glu Lys Glu Asn Arg Glu Leu Glu Lys Ile  
    770                                      775                                      780  
 30 Ile Ala Glu Lys Glu Glu Arg Val Ser Glu Leu Arg His Gln Leu Gln  
    785                                      790                                      795                                      800  
 Ser Arg Gln Gln Leu Arg Ser Arg Arg His Pro Pro Thr Pro Pro Glu  
    805                                      810                                      815  
 35 Pro Ser Gly Gly Leu Pro Arg Gly Pro Pro Glu Pro Pro Asp Arg Leu  
    820                                      825                                      830  
 Ser Cys Asp Gly Ser Arg Val His Leu Leu Tyr Lys  
 40                                      835                                      840

(2) INFORMATION FOR SEQ ID NO: 52:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2895 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Canis familiaris

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..2895

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

ATG CTG CTG CTG CTC CTG CCG CTG GCG CTG GCG CCG CTC TTC CTC CGC	48
Met Leu Leu Leu Leu Leu Pro Leu Ala Leu Ala Pro Leu Phe Leu Arg	
1 5 10 15	
CCC CCG GGC GCG GGC GGG GCA CAG ACC CCC AAC GCC ACC TCG GAA GGT	96
Pro Pro Gly Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly	
20 25 30	
TGC CAG ATC ATA CAC CCG CCT TGG GAA GGG GGT ATC AGG TAC AGG GGC	144
Cys Gln Ile Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly	
35 40 45	
CTG ACT CGT GAC CAG GTG AAG GCT ATC AAC TTC CTG CCG GTG GAC TAT	192
Leu Thr Arg Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr	
50 55 60	
GAG ATT GAG TAT GTG TGC CCG GGA GAG CGA GAG GTG GTG GGG CCC AAG	240
Glu Ile Glu Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys	
65 70 75 80	
GTC CGA AAG TGC CTG GCC AAT GGC TCC TGG ACA GAT ATG GAC ACA CCC	288

	Val	Arg	Lys	Cys	Leu	Ala	Asn	Gly	Ser	Trp	Thr	Asp	Met	Asp	Thr	Pro	
					85					90					95		
	AGC	CGC	TGT	GTC	CGA	ATC	TGT	TCC	AAG	TCA	TAT	TTG	GCC	CTG	GAA	AAT	336
5	Ser	Arg	Cys	Val	Arg	Ile	Cys	Ser	Lys	Ser	Tyr	Leu	Ala	Leu	Glu	Asn	
				100					105					110			
	GGG	AAG	GTC	TTC	CTG	ACG	GGT	GGG	GAC	CTC	CCC	GCT	CTG	GAT	GGA	GCC	384
10	Gly	Lys	Val	Phe	Leu	Thr	Gly	Gly	Asp	Leu	Pro	Ala	Leu	Asp	Gly	Ala	
			115					120					125				
	CGG	GTG	GAT	TTC	CGG	TGT	GAC	CCT	GAC	TTC	CAT	CTT	GTG	GGC	AGC	TCC	432
15	Arg	Val	Asp	Phe	Arg	Cys	Asp	Pro	Asp	Phe	His	Leu	Val	Gly	Ser	Ser	
			130				135					140					
	CGG	AGT	ATC	TGT	AGT	CAG	GGC	CAG	TGG	AGC	ACT	CCC	AAG	CCC	CAC	TGC	480
	Arg	Ser	Ile	Cys	Ser	Gln	Gly	Gln	Trp	Ser	Thr	Pro	Lys	Pro	His	Cys	
	145					150				155					160		
20	CAG	GTG	AGC	CGA	ACG	CCG	CAC	TCA	GAG	CGG	CGA	GCG	GTG	TAC	ATC	GGG	528
	Gln	Val	Ser	Arg	Thr	Pro	His	Ser	Glu	Arg	Arg	Ala	Val	Tyr	Ile	Gly	
					165					170				175			
	GCG	CTG	TTT	CCC	ATG	AGC	GGG	GGC	TGG	CCG	GGG	GGC	CAG	GCC	TGC	CAG	576
25	Ala	Leu	Phe	Pro	Met	Ser	Gly	Gly	Trp	Pro	Gly	Gly	Gln	Ala	Cys	Gln	
				180					185					190			
	CCC	GCG	GTG	GAG	ATG	GCG	CTG	GAG	GAC	GTG	AAT	AGC	CGC	AGG	GAC	ATC	624
30	Pro	Ala	Val	Glu	Met	Ala	Leu	Glu	Asp	Val	Asn	Ser	Arg	Arg	Asp	Ile	
			195					200					205				
	CTG	CCG	GAC	TAC	GAG	CTC	AAG	CTC	ATC	CAC	CAC	GAC	AGC	AAG	TGT	GAC	672
35	Leu	Pro	Asp	Tyr	Glu	Leu	Lys	Leu	Ile	His	His	Asp	Ser	Lys	Cys	Asp	
			210				215					220					
	CCA	GGC	CAA	GCT	ACC	AAG	TAC	CTG	TAT	GAA	CTG	CTC	TAC	AAC	GAC	CCC	720
	Pro	Gly	Gln	Ala	Thr	Lys	Tyr	Leu	Tyr	Glu	Leu	Leu	Tyr	Asn	Asp	Pro	
	225					230				235					240		
40	ATC	AAG	ATC	ATC	CTC	ATG	CCT	GGC	TGC	AGC	TCT	GTC	TCC	ACG	CTT	GTG	768
	Ile	Lys	Ile	Ile	Leu	Met	Pro	Gly	Cys	Ser	Ser	Val	Ser	Thr	Leu	Val	
					245				250					255			

	GCT GAG GCT GCC AGG ATG TGG AAC CTC ATT GTG CTC TCC TAT GGT TCC	816
	Ala Glu Ala Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser	
	260 265 270	
5	AGC TCA CCA GCT CTG TCC AAC CGG CAG CGC TTT CCT ACC TTC TTC CGA	864
	Ser Ser Pro Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg	
	275 280 285	
	ACT CAT CCC TCG GCC ACG CTC CAC AAC CCT ACG CGA GTG AAG CTC TTT	912
10	Thr His Pro Ser Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe	
	290 295 300	
	GAG AAG TGG GGC TGG AGG AAG ATT GCC ACC ATC CAG CAG ACC ACC GAG	960
	Glu Lys Trp Gly Trp Arg Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu	
15	305 310 315 320	
	GTG TTC ACA TCG ACT CTG GAC GAC CTA GAG GAA CGA GTG AAG GAG GCT	1008
	Val Phe Thr Ser Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala	
	325 330 335	
20	GGG ATT GAG ATT ACT TTC CGC CAG AGC TTC TTC TCA GAT CCT GCC GTG	1056
	Gly Ile Glu Ile Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val	
	340 345 350	
25	CCT GTC AAG AAC CTC AAG CGC CAG GAT GCC CGA ATC ATC GTG GGA CTT	1104
	Pro Val Lys Asn Leu Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu	
	355 360 365	
	TTC TAT GAG ACT GAA GCC CGG AAA GTG TTC TGT GAG GTA TAC AAG GAG	1152
30	Phe Tyr Glu Thr Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu	
	370 375 380	
	CGG CTC TTT GGG AAG AAG TAT GTG TGG TTC CTC ATT GGG TGG TAT GCT	1200
	Arg Leu Phe Gly Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala	
35	385 390 395 400	
	GAC AAT TGG TTC AAG ACC TAC GAC CCC TCC ATC AAC TGC ACA GTG GAT	1248
	Asp Asn Trp Phe Lys Thr Tyr Asp Pro Ser Ile Asn Cys Thr Val Asp	
	405 410 415	
40	GAG ATG ACC GAG GCT GTG GAA GGC CAC ATC ACC ACT GAG ATT GTC ATG	1296
	Glu Met Thr Glu Ala Val Glu Gly His Ile Thr Thr Glu Ile Val Met	
	420 425 430	

	CTG AAC CCA GCC AAC ACC CGC AGC ATC TCC AAC ATG ACA TCC CAG GAG	1344
	Leu Asn Pro Ala Asn Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu	
	435 440 445	
5	TTT GTG GAG AAA CTG ACC AAG AGA CTC AAG AGA CAC CCT GAG GAG ACA	1392
	Phe Val Glu Lys Leu Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr	
	450 455 460	
10	GGC GGC TTC CAG GAG GCA CCG CTG GCC TAT GAT GCC ATC TGG GCC TTG	1440
	Gly Gly Phe Gln Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu	
	465 470 475 480	
	GCA TTG GCC CTG AAC AAG ACA TCT GGA GGG AGC GGC CGT TCG GGG GTG	1488
15	Ala Leu Ala Leu Asn Lys Thr Ser Gly Gly Ser Gly Arg Ser Gly Val	
	485 490 495	
	CGC CTG GAA GAC TTC AAC TAC AAC AAC CAG ACG ATC ACA GAC CAA ATC	1536
	Arg Leu Glu Asp Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile	
20	500 505 510	
	TAC CGC GCA ATG AAC TCC TCG TCC TTT GAG GGT GTC TCT GGC CAC GTG	1584
	Tyr Arg Ala Met Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val	
	515 520 525	
25	GTG TTT GAT GCC AGC GGC TCA CGG ATG GCC TGG ACT CTG ATT GAG CAG	1632
	Val Phe Asp Ala Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln	
	530 535 540	
30	CTG CAG GGT GGC AGC TAC AAG AAG ATC GGC TAC TAT GAC AGC ACC AAG	1680
	Leu Gln Gly Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys	
	545 550 555 560	
	GAT GAC CTT TCC TGG TCT AAA ACG GAC AAA TGG ATT GGA GGG GCC CCC	1728
35	Asp Asp Leu Ser Trp Ser Lys Thr Asp Lys Trp Ile Gly Gly Ala Pro	
	565 570 575	
	CCG GCC GAC CAG ACC CTG GTC ATC AAG ACA TTT CGC TTC ATG TCA CAG	1776
	Pro Ala Asp Gln Thr Leu Val Ile Lys Thr Phe Arg Phe Met Ser Gln	
40	580 585 590	
	AAG CTC TTC ATT TCA GTC TCT GTC CTC TCC AGC CTG GGC ATT GTC CTG	1824
	Lys Leu Phe Ile Ser Val Ser Val Leu Ser Ser Leu Gly Ile Val Leu	

	595	600	605	
	GCT GTG GTC TGT CTG TCC TTT AAC ATC TAC AAC TCT CAT GTC CGT TAC			1872
	Ala Val Val Cys Leu Ser Phe Asn Ile Tyr Asn Ser His Val Arg Tyr			
5	610	615	620	
	ATC CAG AAC TCC CAG CCC AAC TTG AAC AAT CTG ACT GCT GTG GGC TGC			1920
	Ile Gln Asn Ser Gln Pro Asn Leu Asn Asn Leu Thr Ala Val Gly Cys			
	625	630	635	640
10				
	TCC CTG GCA TTG GCT GCC GTC TTC CCC CTG GGG CTA GAT GGG TAC CAC			1968
	Ser Leu Ala Leu Ala Ala Val Phe Pro Leu Gly Leu Asp Gly Tyr His			
	645	650	655	
15				
	ATC GGG AGA AGC CAG TTT CCT TTT GTG TGT CAG GCA CGC CTC TGG CTC			2016
	Ile Gly Arg Ser Gln Phe Pro Phe Val Cys Gln Ala Arg Leu Trp Leu			
	660	665	670	
	CTG GGT CTG GGC TTC AGT CTG GGC TAT GGC TCC ATG TTC ACG AAG ATC			2064
20	Leu Gly Leu Gly Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr Lys Ile			
	675	680	685	
	TGG TGG GTC CAC ACG GTC TTC ACT AAG AAG GAG GAG AAG AAG GAG TGG			2112
	Trp Trp Val His Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp			
25	690	695	700	
	AGG AAG ACC CTG GAG CCC TGG AAG CTG TAC ACC ACA GTG GGC TTG CTA			2160
	Arg Lys Thr Leu Glu Pro Trp Lys Leu Tyr Thr Thr Val Gly Leu Leu			
	705	710	715	720
30				
	GTG GGC ATG GAT GTC CTC ACT CTT GCC ATT TGG CAG ATG GTA GAC CCC			2208
	Val Gly Met Asp Val Leu Thr Leu Ala Ile Trp Gln Met Val Asp Pro			
	725	730	735	
35				
	TTG CAC CGG ACC ATT GAG ACT TTT GCC AAG GAG GAA CCA AAG GAA GAT			2256
	Leu His Arg Thr Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys Glu Asp			
	740	745	750	
	ATT GAT GTG TCC ATC CTG CCC CAG CTG GAG CAC TGC AGC TCC AAG AAA			2304
40	Ile Asp Val Ser Ile Leu Pro Gln Leu Glu His Cys Ser Ser Lys Lys			
	755	760	765	
	ATG AAC ACC TGG CTT GGC ATT TTC TAT GGT TAC AAG GGG CTG CTG CTG			2352



	Met	Asn	Thr	Trp	Leu	Gly	Ile	Phe	Tyr	Gly	Tyr	Lys	Gly	Leu	Leu	Leu	
	770						775					780					
	CTG	CTA	GGC	ATC	TTT	CTT	GCT	TAT	GAG	ACC	AAG	AGC	GTG	TCT	ACT	GAG	2400
5	Leu	Leu	Gly	Ile	Phe	Leu	Ala	Tyr	Glu	Thr	Lys	Ser	Val	Ser	Thr	Glu	
	785					790					795					800	
	AAG	ATC	AAT	GAC	CAC	CGG	GCT	GTG	GGC	ATG	GCC	ATG	TAC	AAC	GTG	GCG	2448
	Lys	Ile	Asn	Asp	His	Arg	Ala	Val	Gly	Met	Ala	Met	Tyr	Asn	Val	Ala	
10					805					810					815		
	GTC	CTG	TGC	CTC	ATC	ACT	GCC	CCG	GTC	ACC	ATG	ATC	CTG	TCC	AGC	CAG	2496
	Val	Leu	Cys	Leu	Ile	Thr	Ala	Pro	Val	Thr	Met	Ile	Leu	Ser	Ser	Gln	
					820					825					830		
15																	
	CAG	GAT	GCA	GCT	TTC	GCC	TTT	GCA	GCT	CTT	GCC	ATA	GTG	TTC	TCC	TCC	2544
	Gln	Asp	Ala	Ala	Phe	Ala	Phe	Ala	Ala	Leu	Ala	Ile	Val	Phe	Ser	Ser	
					835					840					845		
20	TAC	ATC	ACT	CTG	GTC	GTT	CTG	TTC	GTG	CCG	AAG	ATG	CGC	AGG	TTG	ATC	2592
	Tyr	Ile	Thr	Leu	Val	Val	Leu	Phe	Val	Pro	Lys	Met	Arg	Arg	Leu	Ile	
					850					855					860		
	ACC	CGG	GGT	GAG	TGG	CAG	TCG	GAG	GCG	CAG	GAT	ACC	ATG	AAA	ACG	GGG	2640
25	Thr	Arg	Gly	Glu	Trp	Gln	Ser	Glu	Ala	Gln	Asp	Thr	Met	Lys	Thr	Gly	
					865						870				875		880
	TCG	TCG	ACC	AAC	AAC	AAT	GAG	GAA	GAG	AAG	TCC	CGA	CTG	TTG	GAG	AAG	2688
	Ser	Ser	Thr	Asn	Asn	Asn	Glu	Glu	Glu	Lys	Ser	Arg	Leu	Leu	Glu	Lys	
30					885					890					895		
	GAG	AAC	CGG	GAG	CTG	GAG	AAG	ATC	ATT	GCT	GAG	AAA	GAG	GAG	CGA	GTG	2736
	Glu	Asn	Arg	Glu	Leu	Glu	Lys	Ile	Ile	Ala	Glu	Lys	Glu	Glu	Arg	Val	
					900					905					910		
35																	
	TCC	GAG	CTG	CGC	CAT	CAG	CTT	CGT	TCT	CGG	CAG	CAG	CTG	CGC	CCT	CGG	2784
	Ser	Glu	Leu	Arg	His	Gln	Leu	Arg	Ser	Arg	Gln	Gln	Leu	Arg	Pro	Arg	
					915					920					925		
40	CGT	CAC	CCC	CCG	ACG	CCC	CCA	GAC	CCC	TCA	GGG	GGC	CTG	CCC	AGG	GGA	2832
	Arg	His	Pro	Pro	Thr	Pro	Pro	Asp	Pro	Ser	Gly	Gly	Leu	Pro	Arg	Gly	
					930					935					940		

CCC CAT GAG CCC CCT GAC CGG CTC AGC TGT GAC GGG AGC CGG GTT CAC 2880  
 Pro His Glu Pro Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg Val His  
 945 950 955 960

5 TTG CTG TAC AAG TGA 2895  
 Leu Leu Tyr Lys \*  
 965

10 (2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 964 amino acids  
 (B) TYPE: amino acid  
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

20 Met Leu Leu Leu Leu Leu Pro Leu Ala Leu Ala Pro Leu Phe Leu Arg  
 1 5 10 15  
 Pro Pro Gly Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly  
 25 20 25 30  
 Cys Gln Ile Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly  
 35 40 45  
 30 Leu Thr Arg Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr  
 50 55 60  
 Glu Ile Glu Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys  
 65 70 75 80  
 35 Val Arg Lys Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro  
 85 90 95  
 Ser Arg Cys Val Arg Ile Cys Ser Lys Ser Tyr Leu Ala Leu Glu Asn  
 40 100 105 110  
 Gly Lys Val Phe Leu Thr Gly Gly Asp Leu Pro Ala Leu Asp Gly Ala  
 115 120 125

Arg Val Asp Phe Arg Cys Asp Pro Asp Phe His Leu Val Gly Ser Ser  
 130 135 140

5 Arg Ser Ile Cys Ser Gln Gly Gln Trp Ser Thr Pro Lys Pro His Cys  
 145 150 155 160

Gln Val Ser Arg Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly  
 165 170 175

10 Ala Leu Phe Pro Met Ser Gly Gly Trp Pro Gly Gly Gln Ala Cys Gln  
 180 185 190

Pro Ala Val Glu Met Ala Leu Glu Asp Val Asn Ser Arg Arg Asp Ile  
 15 195 200 205

Leu Pro Asp Tyr Glu Leu Lys Leu Ile His His Asp Ser Lys Cys Asp  
 210 215 220

20 Pro Gly Gln Ala Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro  
 225 230 235 240

Ile Lys Ile Ile Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val  
 245 250 255

25 Ala Glu Ala Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser  
 260 265 270

Ser Ser Pro Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg  
 30 275 280 285

Thr His Pro Ser Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe  
 290 295 300

35 Glu Lys Trp Gly Trp Arg Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu  
 305 310 315 320

Val Phe Thr Ser Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala  
 325 330 335

40 Gly Ile Glu Ile Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val  
 340 345 350

Pro Val Lys Asn Leu Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu  
 355 360 365

Phe Tyr Glu Thr Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu  
 5 370 375 380

Arg Leu Phe Gly Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala  
 385 390 395 400

10 Asp Asn Trp Phe Lys Thr Tyr Asp Pro Ser Ile Asn Cys Thr Val Asp  
 405 410 415

Glu Met Thr Glu Ala Val Glu Gly His Ile Thr Thr Glu Ile Val Met  
 420 425 430

15 Leu Asn Pro Ala Asn Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu  
 435 440 445

Phe Val Glu Lys Leu Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr  
 20 450 455 460

Gly Gly Phe Gln Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu  
 465 470 475 480

25 Ala Leu Ala Leu Asn Lys Thr Ser Gly Gly Ser Gly Arg Ser Gly Val  
 485 490 495

Arg Leu Glu Asp Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile  
 500 505 510

30 Tyr Arg Ala Met Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val  
 515 520 525

Val Phe Asp Ala Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln  
 35 530 535 540

Leu Gln Gly Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys  
 545 550 555 560

40 Asp Asp Leu Ser Trp Ser Lys Thr Asp Lys Trp Ile Gly Gly Ala Pro  
 565 570 575

Pro Ala Asp Gln Thr Leu Val Ile Lys Thr Phe Arg Phe Met Ser Gln

	580	585	590
	Lys Leu Phe Ile Ser Val Ser Val Leu Ser Ser Leu Gly Ile Val Leu		
	595	600	605
5	Ala Val Val Cys Leu Ser Phe Asn Ile Tyr Asn Ser His Val Arg Tyr		
	610	615	620
	Ile Gln Asn Ser Gln Pro Asn Leu Asn Asn Leu Thr Ala Val Gly Cys		
10	625	630	635 640
	Ser Leu Ala Leu Ala Ala Val Phe Pro Leu Gly Leu Asp Gly Tyr His		
	645	650	655
15	Ile Gly Arg Ser Gln Phe Pro Phe Val Cys Gln Ala Arg Leu Trp Leu		
	660	665	670
	Leu Gly Leu Gly Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr Lys Ile		
	675	680	685
20	Trp Trp Val His Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp		
	690	695	700
	Arg Lys Thr Leu Glu Pro Trp Lys Leu Tyr Thr Thr Val Gly Leu Leu		
25	705	710	715 720
	Val Gly Met Asp Val Leu Thr Leu Ala Ile Trp Gln Met Val Asp Pro		
	725	730	735
30	Leu His Arg Thr Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys Glu Asp		
	740	745	750
	Ile Asp Val Ser Ile Leu Pro Gln Leu Glu His Cys Ser Ser Lys Lys		
	755	760	765
35	Met Asn Thr Trp Leu Gly Ile Phe Tyr Gly Tyr Lys Gly Leu Leu Leu		
	770	775	780
	Leu Leu Gly Ile Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser Thr Glu		
40	785	790	795 800
	Lys Ile Asn Asp His Arg Ala Val Gly Met Ala Met Tyr Asn Val Ala		
	805	810	815

Val Leu Cys Leu Ile Thr Ala Pro Val Thr Met Ile Leu Ser Ser Gln  
820 825 830

5 Gln Asp Ala Ala Phe Ala Phe Ala Ala Leu Ala Ile Val Phe Ser Ser  
835 840 845

Tyr Ile Thr Leu Val Val Leu Phe Val Pro Lys Met Arg Arg Leu Ile  
850 855 860

10 Thr Arg Gly Glu Trp Gln Ser Glu Ala Gln Asp Thr Met Lys Thr Gly  
865 870 875 880

Ser Ser Thr Asn Asn Asn Glu Glu Glu Lys Ser Arg Leu Leu Glu Lys  
15 885 890 895

Glu Asn Arg Glu Leu Glu Lys Ile Ile Ala Glu Lys Glu Glu Arg Val  
900 905 910

20 Ser Glu Leu Arg His Gln Leu Arg Ser Arg Gln Gln Leu Arg Pro Arg  
915 920 925

Arg His Pro Pro Thr Pro Pro Asp Pro Ser Gly Gly Leu Pro Arg Gly  
930 935 940

25 Pro His Glu Pro Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg Val His  
945 950 955 960

Leu Leu Tyr Lys

30

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1737 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

5

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..1737

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

ATG TTG CTG CTG CTG CTA CTG GCG CCA CTC TTC CTC CGC CCC CCG GGC	48
Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly	
1 5 10 15	
GCG GGC GGG GCG CAG ACC CCC AAC GCC ACC TCA GAA GGT TGC CAG ATC	96
Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile	
20 25 30	
ATA CAC CCG CCC TGG GAA GGG GGC ATC AGG TAC CGG GGC CTG ACT CGG	144
Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg	
35 40 45	
GAC CAG GTG AAG GCT ATC AAC TTC CTG CCA GTG GAC TAT GAG ATT GAG	192
Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu	
50 55 60	
TAT GTG TGC CGG GGG GAG CGC GAG GTG GTG GGG CCC AAG GTC CGC AAG	240
Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys	
65 70 75 80	
TGC CTG GCC AAC GGC TCC TGG ACA GAT ATG GAC ACA CCC AGC CGC TGT	288
Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys	
85 90 95	
GTC CGA ATC TGC TCC AAG TCT TAT TTG ACC CTG GAA AAT GGG AAG GTT	336
Val Arg Ile Cys Ser Lys Ser Tyr Leu Thr Leu Glu Asn Gly Lys Val	
100 105 110	
TTC CTG ACG GGT GGG GAC CTC CCA GCT CTG GAC GGA GCC CGG GTG GAT	384
Phe Leu Thr Gly Gly Asp Leu Pro Ala Leu Asp Gly Ala Arg Val Asp	
115 120 125	

	TTC CGG TGT GAC CCC GAC TTC CAT CTG GTG GGC AGC TCC CGG AGC ATC	432
	Phe Arg Cys Asp Pro Asp Phe His Leu Val Gly Ser Ser Arg Ser Ile	
	130 135 140	
5	TGT AGT CAG GGC CAG TGG AGC ACC CCC AAG CCC CAC TGC CAG GTG AAT	480
	Cys Ser Gln Gly Gln Trp Ser Thr Pro Lys Pro His Cys Gln Val Asn	
	145 150 155 160	
	CGA ACG CCA CAC TCA GAA CGG CGC GCA GTG TAC ATC GGG GCA CTG TTT	528
10	Arg Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe	
	165 170 175	
	CCC ATG AGC GGG GGC TGG CCA GGG GGC CAG GCC TGC CAG CCC GCG GTG	576
	Pro Met Ser Gly Gly Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val	
15	180 185 190	
	GAG ATG GCG CTG GAG GAC GTG AAT AGC CGC AGG GAC ATC CTG CCG GAC	624
	Glu Met Ala Leu Glu Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp	
	195 200 205	
20	TAT GAG CTC AAG CTC ATC CAC CAC GAC AGC AAG TGT GAT CCA GGC CAA	672
	Tyr Glu Leu Lys Leu Ile His His Asp Ser Lys Cys Asp Pro Gly Gln	
	210 215 220	
25	GCC ACC AAG TAC CTA TAT GAG CTG CTC TAC AAC GAC CCT ATC AAG ATC	720
	Ala Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile	
	225 230 235 240	
	ATC CTT ATG CCT GGC TGC AGC TCT GTC TCC ACG CTG GTG GCT GAG GCT	768
30	Ile Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala	
	245 250 255	
	GCT AGG ATG TGG AAC CTC ATT GTG CTT TCC TAT GGC TCC AGC TCA CCA	816
	Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro	
35	260 265 270	
	GCC CTG TCA AAC CGG CAG CGT TTC CCC ACT TTC TTC CGA ACG CAC CCA	864
	Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro	
	275 280 285	
40	TCA GCC ACA CTC CAC AAC CCT ACC CGC GTG AAA CTC TTT GAA AAG TGG	912
	Ser Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp	
	290 295 300	



	GGC TGG AAG AAG ATT GCT ACC ATC CAG CAG ACC ACT GAG GTC TTC ACT	960
	Gly Trp Lys Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr	
	305 310 315 320	
5	TCG ACT CTG GAC GAC CTG GAG GAA CGA GTG AAG GAG GCT GGA ATT GAG	1008
	Ser Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu	
	325 330 335	
10	ATT ACT TTC CGC CAG AGT TTC TTC TCA GAT CCA GCT GTG CCC GTC AAA	1056
	Ile Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys	
	340 345 350	
	AAC CTG AAG CGC CAG GAT GCC CGA ATC ATC GTG GGA CTT TTC TAT GAG	1104
15	Asn Leu Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu	
	355 360 365	
	ACT GAA GCC CGG AAA GTT TTT TGT GAG GTG TAC AAG GAG CGT CTC TTT	1152
	Thr Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe	
20	370 375 380	
	GGG AAG AAG TAC GTC TGG TTC CTC ATT GGG TGG TAT GCT GAC AAT TGG	1200
	Gly Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp	
	385 390 395 400	
25	TTC AAG ATC TAC GAC CCT TCT ATC AAC TGC ACA GTG GAT GAG ATG ACT	1248
	Phe Lys Ile Tyr Asp Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr	
	405 410 415	
30	GAG GCG GTG GAG GGC CAC ATC ACA ACT GAG ATT GTC ATG CTG AAT CCT	1296
	Glu Ala Val Glu Gly His Ile Thr Thr Glu Ile Val Met Leu Asn Pro	
	420 425 430	
	GCC AAT ACC CGC AGC ATT TCC AAC ATG ACA TCC CAG GAA TTT GTG GAG	1344
35	Ala Asn Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu	
	435 440 445	
	AAA CTA ACC AAG CGA CTG AAA AGA CAC CCT GAG GAG ACA GGA GGC TTC	1392
	Lys Leu Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe	
40	450 455 460	
	CAG GAG GCA CCG CTG GCC TAT GAT GCC ATC TGG GCC TTG GCA CTG GCC	1440
	Gln Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala	

	465		470		475		480	
	CTG AAC AAG ACA TCT GGA GGA GGC GGC CGT TCT GGT GTG CGC CTG GAG	1488						
	Leu Asn Lys Thr Ser Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu							
5		485	490	495				
	GAC TTC AAC TAC AAC AAC CAG ACC ATT ACC GAC CAA ATC TAC CGG GCA	1536						
	Asp Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala							
		500	505	510				
10								
	ATG AAC TCT TCG TCC TTT GAG GGT GTC TCT GGC CAT GTG GTG TTT GAT	1584						
	Met Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val Val Phe Asp							
		515	520	525				
15								
	GCC AGC GGC TCT CGG ATG GCA TGG ACG CTT ATC GAG CAG CTT CAG GGT	1632						
	Ala Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly							
		530	535	540				
	GGC AGC TAC AAG AAG ATT GGC TAC TAT GAC AGC ACC AAG GAT GAT CTT	1680						
20	Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu							
		545	550	555	560			
	TCC TGG TCC AAA ACA GAT AAA TGG ATT GTT ATA TCC AGA ACT CAC AGC	1728						
	Ser Trp Ser Lys Thr Asp Lys Trp Ile Val Ile Ser Arg Thr His Ser							
25		565	570	575				
	CCA ACC TGA				1737			
	Pro Thr *							

30

(2) INFORMATION FOR SEQ ID NO: 55:

## (i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 578 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly

1                      5                      10                      15  
 Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile  
                          20                      25                      30  
 5  
 Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg  
                          35                      40                      45  
 Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu  
 10                      50                      55                      60  
 Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys  
                          65                      70                      75                      80  
 15    Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys  
    85                      90                      95  
 Val Arg Ile Cys Ser Lys Ser Tyr Leu Thr Leu Glu Asn Gly Lys Val  
    100                      105                      110  
 20  
 Phe Leu Thr Gly Gly Asp Leu Pro Ala Leu Asp Gly Ala Arg Val Asp  
    115                      120                      125  
 Phe Arg Cys Asp Pro Asp Phe His Leu Val Gly Ser Ser Arg Ser Ile  
 25                      130                      135                      140  
 Cys Ser Gln Gly Gln Trp Ser Thr Pro Lys Pro His Cys Gln Val Asn  
    145                      150                      155                      160  
 30    Arg Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe  
    165                      170                      175  
 Pro Met Ser Gly Gly Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val  
    180                      185                      190  
 35  
 Glu Met Ala Leu Glu Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp  
    195                      200                      205  
 Tyr Glu Leu Lys Leu Ile His His Asp Ser Lys Cys Asp Pro Gly Gln  
 40                      210                      215                      220  
 Ala Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile  
    225                      230                      235                      240

Ile Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala  
 245 250 255

5 Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro  
 260 265 270

Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro  
 275 280 285

10 Ser Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp  
 290 295 300

Gly Trp Lys Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr  
 15 305 310 315 320

Ser Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu  
 325 330 335

20 Ile Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys  
 340 345 350

Asn Leu Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu  
 355 360 365

25 Thr Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe  
 370 375 380

Gly Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp  
 30 385 390 395 400

Phe Lys Ile Tyr Asp Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr  
 405 410 415

35 Glu Ala Val Glu Gly His Ile Thr Thr Glu Ile Val Met Leu Asn Pro  
 420 425 430

Ala Asn Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu  
 435 440 445

40 Lys Leu Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe  
 450 455 460

Gln Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala  
 465 470 475 480  
 Leu Asn Lys Thr Ser Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu  
 5 485 490 495  
 Asp Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala  
 500 505 510  
 10 Met Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val Val Phe Asp  
 515 520 525  
 Ala Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly  
 530 535 540  
 15 Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu  
 545 550 555 560  
 Ser Trp Ser Lys Thr Asp Lys Trp Ile Val Ile Ser Arg Thr His Ser  
 20 565 570 575  
 Pro Thr

25

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1386 base pairs  
 30 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..1386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

5	ATG GGG CCC GGG GCC CCT TTT GCC CGG GTG GGG TGG CCA CTG CCG CTT	48
	Met Gly Pro Gly Ala Pro Phe Ala Arg Val Gly Trp Pro Leu Pro Leu	
	1 5 10 15	
10	CTG GTT GTG ATG GCG GCA GGG GTG GCT CCG GTG TGG GCC TCC CAC TCC	96
	Leu Val Val Met Ala Ala Gly Val Ala Pro Val Trp Ala Ser His Ser	
	20 25 30	
	CCC CAT CTC CCG CGG CCT CAC TCG CGG GTC CCC CCG CAC CCC TCC TCA	144
15	Pro His Leu Pro Arg Pro His Ser Arg Val Pro Pro His Pro Ser Ser	
	35 40 45	
	GAA CGG CGC GCA GTG TAC ATC GGG GCA CTG TTT CCC ATG AGC GGG GGC	192
20	Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe Pro Met Ser Gly Gly	
	50 55 60	
	TGG CCA GGG GGC CAG GCC TGC CAG CCC GCG GTG GAG ATG GCG CTG GAG	240
	Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val Glu Met Ala Leu Glu	
	65 70 75 80	
25	GAC GTG AAT AGC CGC AGG GAC ATC CTG CCG GAC TAT GAG CTC AAG CTC	288
	Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp Tyr Glu Leu Lys Leu	
	85 90 95	
30	ATC CAC CAC GAC AGC AAG TGT GAT CCA GGC CAA GCC ACC AAG TAC CTA	336
	Ile His His Asp Ser Lys Cys Asp Pro Gly Gln Ala Thr Lys Tyr Leu	
	100 105 110	
	TAT GAG CTG CTC TAC AAC GAC CCT ATC AAG ATC ATC CTT ATG CCT GGC	384
35	Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile Ile Leu Met Pro Gly	
	115 120 125	
	TGC AGC TCT GTC TCC ACG CTG GTG GCT GAG GCT GCT AGG ATG TGG AAC	432
40	Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala Arg Met Trp Asn	
	130 135 140	
	CTC ATT GTG CTT TCC TAT GGC TCC AGC TCA CCA GCC CTG TCA AAC CGG	480
	Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala Leu Ser Asn Arg	

	145	150	155	160	
	CAG CGT TTC CCC ACT TTC TTC CGA ACG CAC CCA TCA GCC ACA CTC CAC				528
	Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro Ser Ala Thr Leu His				
5		165	170	175	
	AAC CCT ACC CGC GTG AAA CTC TTT GAA AAG TGG GGC TGG AAG AAG ATT				576
	Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp Gly Trp Lys Lys Ile				
		180	185	190	
10	GCT ACC ATC CAG CAG ACC ACT GAG GTC TTC ACT TCG ACT CTG GAC GAC				624
	Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr Ser Thr Leu Asp Asp				
		195	200	205	
15	CTG GAG GAA CGA GTG AAG GAG GCT GGA ATT GAG ATT ACT TTC CGC CAG				672
	Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu Ile Thr Phe Arg Gln				
		210	215	220	
	AGT TTC TTC TCA GAT CCA GCT GTG CCC GTC AAA AAC CTG AAG CGC CAG				720
20	Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys Asn Leu Lys Arg Gln				
		225	230	235	240
	GAT GCC CGA ATC ATC GTG GGA CTT TTC TAT GAG ACT GAA GCC CGG AAA				768
	Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu Thr Glu Ala Arg Lys				
25		245	250	255	
	GTT TTT TGT GAG GTG TAC AAG GAG CGT CTC TTT GGG AAG AAG TAC GTC				816
	Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly Lys Lys Tyr Val				
		260	265	270	
30	TGG TTC CTC ATT GGG TGG TAT GCT GAC AAT TGG TTC AAG ATC TAC GAC				864
	Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe Lys Ile Tyr Asp				
		275	280	285	
35	CCT TCT ATC AAC TGC ACA GTG GAT GAG ATG ACT GAG GCG GTG GAG GGC				912
	Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr Glu Ala Val Glu Gly				
		290	295	300	
	CAC ATC ACA ACT GAG ATT GTC ATG CTG AAT CCT GCC AAT ACC CGC AGC				960
40	His Ile Thr Thr Glu Ile Val Met Leu Asn Pro Ala Asn Thr Arg Ser				
		305	310	315	320
	ATT TCC AAC ATG ACA TCC CAG GAA TTT GTG GAG AAA CTA ACC AAG CGA				1008

Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu Lys Leu Thr Lys Arg  
 325 330 335

CTG AAA AGA CAC CCT GAG GAG ACA GGA GGC TTC CAG GAG GCA CCG CTG 1056  
 5 Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln Glu Ala Pro Leu  
 340 345 350

GCC TAT GAT GCC ATC TGG GCC TTG GCA CTG GCC CTG AAC AAG ACA TCT 1104  
 10 Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Leu Asn Lys Thr Ser  
 355 360 365

GGA GGA GGC GGC CGT TCT GGT GTG CGC CTG GAG GAC TTC AAC TAC AAC 1152  
 Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu Asp Phe Asn Tyr Asn  
 370 375 380

15 AAC CAG ACC ATT ACC GAC CAA ATC TAC CGG GCA ATG AAC TCT TCG TCC 1200  
 Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala Met Asn Ser Ser Ser  
 385 390 395 400

20 TTT GAG GGT GTC TCT GGC CAT GTG GTG TTT GAT GCC AGC GGC TCT CGG 1248  
 Phe Glu Gly Val Ser Gly His Val Val Phe Asp Ala Ser Gly Ser Arg  
 405 410 415

ATG GCA TGG ACG CTT ATC GAG CAG CTT CAG GGT GGC AGC TAC AAG AAG 1296  
 25 Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly Gly Ser Tyr Lys Lys  
 420 425 430

ATT GGC TAC TAT GAC AGC ACC AAG GAT GAT CTT TCC TGG TCC AAA ACA 1344  
 Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu Ser Trp Ser Lys Thr  
 30 435 440 445

GAT AAA TGG ATT GTT ATA TCC AGA ACT CAC AGC CCA ACC TGA 1386  
 Asp Lys Trp Ile Val Ile Ser Arg Thr His Ser Pro Thr \*  
 450 455 460

35

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 461 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

Met Gly Pro Gly Ala Pro Phe Ala Arg Val Gly Trp Pro Leu Pro Leu  
 5        1                                5                                10                                15

Leu Val Val Met Ala Ala Gly Val Ala Pro Val Trp Ala Ser His Ser  
                              20                                25                                30

10    Pro His Leu Pro Arg Pro His Ser Arg Val Pro Pro His Pro Ser Ser  
                              35                                40                                45

Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe Pro Met Ser Gly Gly  
                              50                                55                                60

15    Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val Glu Met Ala Leu Glu  
                              65                                70                                75                                80

Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp Tyr Glu Leu Lys Leu  
 20                                85                                90                                95

Ile His His Asp Ser Lys Cys Asp Pro Gly Gln Ala Thr Lys Tyr Leu  
                              100                                105                                110

25    Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile Ile Leu Met Pro Gly  
                              115                                120                                125

Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala Arg Met Trp Asn  
                              130                                135                                140

30    Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala Leu Ser Asn Arg  
                              145                                150                                155                                160

Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro Ser Ala Thr Leu His  
 35                                165                                170                                175

Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp Gly Trp Lys Lys Ile  
                              180                                185                                190

40    Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr Ser Thr Leu Asp Asp  
                              195                                200                                205

Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu Ile Thr Phe Arg Gln

	210	215	220	
	Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys Asn Leu Lys Arg Gln			
	225	230	235	240
5	Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu Thr Glu Ala Arg Lys			
	245	250	255	
	Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly Lys Lys Tyr Val			
10	260	265	270	
	Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe Lys Ile Tyr Asp			
	275	280	285	
15	Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr Glu Ala Val Glu Gly			
	290	295	300	
	His Ile Thr Thr Glu Ile Val Met Leu Asn Pro Ala Asn Thr Arg Ser			
	305	310	315	320
20	Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu Lys Leu Thr Lys Arg			
	325	330	335	
	Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln Glu Ala Pro Leu			
25	340	345	350	
	Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Leu Asn Lys Thr Ser			
	355	360	365	
30	Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu Asp Phe Asn Tyr Asn			
	370	375	380	
	Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala Met Asn Ser Ser Ser			
	385	390	395	400
35	Phe Glu Gly Val Ser Gly His Val Val Phe Asp Ala Ser Gly Ser Arg			
	405	410	415	
	Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly Gly Ser Tyr Lys Lys			
40	420	425	430	
	Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu Ser Trp Ser Lys Thr			
	435	440	445	

Asp Lys Trp Ile Val Ile Ser Arg Thr His Ser Pro Thr  
 450 455 460

5

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1746 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Canis familiaris

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..1746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

30	ATG CTG CTG CTG CTC CTG CCG CTG GCG CTG GCG CCG CTC TTC CTC CGC	48
	Met Leu Leu Leu Leu Leu Pro Leu Ala Leu Ala Pro Leu Phe Leu Arg	
	1 5 10 15	
35	CCC CCG GGC GCG GGC GGG GCA CAG ACC CCC AAC GCC ACC TCG GAA GGT	96
	Pro Pro Gly Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly	
	20 25 30	
40	TGC CAG ATC ATA CAC CCG CCT TGG GAA GGG GGT ATC AGG TAC AGG GGC	144
	Cys Gln Ile Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly	
	35 40 45	
	CTG ACT CGT GAC CAG GTG AAG GCT ATC AAC TTC CTG CCG GTG GAC TAT	192
	Leu Thr Arg Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr	
	50 55 60	

	GAG ATT GAG TAT GTG TGC CGG GGA GAG CGA GAG GTG GTG GGG CCC AAG	240
	Glu Ile Glu Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys	
	65 70 75 80	
5	GTC CGA AAG TGC CTG GCC AAT GGC TCC TGG ACA GAT ATG GAC ACA CCC	288
	Val Arg Lys Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro	
	85 90 95	
10	AGC CGC TGT GTC CGA ATC TGT TCC AAG TCA TAT TTG GCC CTG GAA AAT	336
	Ser Arg Cys Val Arg Ile Cys Ser Lys Ser Tyr Leu Ala Leu Glu Asn	
	100 105 110	
	GGG AAG GTC TTC CTG ACG GGT GGG GAC CTC CCC GCT CTG GAT GGA GCC	384
15	Gly Lys Val Phe Leu Thr Gly Gly Asp Leu Pro Ala Leu Asp Gly Ala	
	115 120 125	
	CGG GTG GAT TTC CGG TGT GAC CCT GAC TTC CAT CTT GTG GGC AGC TCC	432
	Arg Val Asp Phe Arg Cys Asp Pro Asp Phe His Leu Val Gly Ser Ser	
20	130 135 140	
	CGG AGT ATC TGT AGT CAG GGC CAG TGG AGC ACT CCC AAG CCC CAC TGC	480
	Arg Ser Ile Cys Ser Gln Gly Gln Trp Ser Thr Pro Lys Pro His Cys	
	145 150 155 160	
25	CAG GTG AGC CGA ACG CCG CAC TCA GAG CGG CGA GCG GTG TAC ATC GGG	528
	Gln Val Ser Arg Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly	
	165 170 175	
30	GCG CTG TTT CCC ATG AGC GGG GGC TGG CCG GGG GGC CAG GCC TGC CAG	576
	Ala Leu Phe Pro Met Ser Gly Gly Trp Pro Gly Gly Gln Ala Cys Gln	
	180 185 190	
	CCC GCG GTG GAG ATG GCG CTG GAG GAC GTG AAT AGC CGC AGG GAC ATC	624
35	Pro Ala Val Glu Met Ala Leu Glu Asp Val Asn Ser Arg Arg Asp Ile	
	195 200 205	
	CTG CCG GAC TAC GAG CTC AAG CTC ATC CAC CAC GAC AGC AAG TGT GAC	672
	Leu Pro Asp Tyr Glu Leu Lys Leu Ile His His Asp Ser Lys Cys Asp	
40	210 215 220	
	CCA GGC CAA GCT ACC AAG TAC CTG TAT GAA CTG CTC TAC AAC GAC CCC	720
	Pro Gly Gln Ala Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro	

	225		230		235		240	
	ATC AAG ATC ATC CTC ATG CCT GGC TGC AGC TCT GTC TCC ACG CTT GTG							768
	Ile Lys Ile Ile Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val							
5		245		250		255		
	GCT GAG GCT GCC AGG ATG TGG AAC CTC ATT GTG CTC TCC TAT GGT TCC							816
	Ala Glu Ala Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser							
		260		265		270		
10								
	AGC TCA CCA GCT CTG TCC AAC CGG CAG CGC TTT CCT ACC TTC TTC CGA							864
	Ser Ser Pro Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg							
		275		280		285		
15								
	ACT CAT CCC TCG GCC ACG CTC CAC AAC CCT ACG CGA GTG AAG CTC TTT							912
	Thr His Pro Ser Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe							
		290		295		300		
	GAG AAG TGG GGC TGG AGG AAG ATT GCC ACC ATC CAG CAG ACC ACC GAG							960
20	Glu Lys Trp Gly Trp Arg Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu							
		305		310		315		320
	GTG TTC ACA TCG ACT CTG GAC GAC CTA GAG GAA CGA GTG AAG GAG GCT							1008
	Val Phe Thr Ser Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala							
25		325		330		335		
	GGG ATT GAG ATT ACT TTC CGC CAG AGC TTC TTC TCA GAT CCT GCC GTG							1056
	Gly Ile Glu Ile Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val							
		340		345		350		
30								
	CCT GTC AAG AAC CTC AAG CGC CAG GAT GCC CGA ATC ATC GTG GGA CTT							1104
	Pro Val Lys Asn Leu Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu							
		355		360		365		
35								
	TTC TAT GAG ACT GAA GCC CGG AAA GTG TTC TGT GAG GTA TAC AAG GAG							1152
	Phe Tyr Glu Thr Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu							
		370		375		380		
	CGG CTC TTT GGG AAG AAG TAT GTG TGG TTC CTC ATT GGG TGG TAT GCT							1200
40	Arg Leu Phe Gly Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala							
		385		390		395		400
	GAC AAT TGG TTC AAG ACC TAC GAC CCC TCC ATC AAC TGC ACA GTG GAT							1248

	Asp	Asn	Trp	Phe	Lys	Thr	Tyr	Asp	Pro	Ser	Ile	Asn	Cys	Thr	Val	Asp	
					405					410					415		
	GAG	ATG	ACC	GAG	GCT	GTG	GAA	GGC	CAC	ATC	ACC	ACT	GAG	ATT	GTC	ATG	1296
5	Glu	Met	Thr	Glu	Ala	Val	Glu	Gly	His	Ile	Thr	Thr	Glu	Ile	Val	Met	
					420					425					430		
	CTG	AAC	CCA	GCC	AAC	ACC	CGC	AGC	ATC	TCC	AAC	ATG	ACA	TCC	CAG	GAG	1344
	Leu	Asn	Pro	Ala	Asn	Thr	Arg	Ser	Ile	Ser	Asn	Met	Thr	Ser	Gln	Glu	
10					435					440					445		
	TTT	GTG	GAG	AAA	CTG	ACC	AAG	AGA	CTC	AAG	AGA	CAC	CCT	GAG	GAG	ACA	1392
	Phe	Val	Glu	Lys	Leu	Thr	Lys	Arg	Leu	Lys	Arg	His	Pro	Glu	Glu	Thr	
					450					455					460		
15																	
	GGC	GGC	TTC	CAG	GAG	GCA	CCG	CTG	GCC	TAT	GAT	GCC	ATC	TGG	GCC	TTG	1440
	Gly	Gly	Phe	Gln	Glu	Ala	Pro	Leu	Ala	Tyr	Asp	Ala	Ile	Trp	Ala	Leu	
					465					470					475		480
	GCA	TTG	GCC	CTG	AAC	AAG	ACA	TCT	GGA	GGG	AGC	GGC	CGT	TCG	GGG	GTG	1488
20	Ala	Leu	Ala	Leu	Asn	Lys	Thr	Ser	Gly	Gly	Ser	Gly	Arg	Ser	Gly	Val	
					485					490					495		
	CGC	CTG	GAA	GAC	TTC	AAC	TAC	AAC	AAC	CAG	ACG	ATC	ACA	GAC	CAA	ATC	1536
25	Arg	Leu	Glu	Asp	Phe	Asn	Tyr	Asn	Asn	Gln	Thr	Ile	Thr	Asp	Gln	Ile	
					500					505					510		
	TAC	CGC	GCA	ATG	AAC	TCC	TCG	TCC	TTT	GAG	GGT	GTC	TCT	GGC	CAC	GTG	1584
	Tyr	Arg	Ala	Met	Asn	Ser	Ser	Ser	Phe	Glu	Gly	Val	Ser	Gly	His	Val	
30					515					520					525		
	GTG	TTT	GAT	GCC	AGC	GGC	TCA	CGG	ATG	GCC	TGG	ACT	CTG	ATT	GAG	CAG	1632
	Val	Phe	Asp	Ala	Ser	Gly	Ser	Arg	Met	Ala	Trp	Thr	Leu	Ile	Glu	Gln	
					530					535					540		
35																	
	CTG	CAG	GGT	GGC	AGC	TAC	AAG	AAG	ATC	GGC	TAC	TAT	GAC	AGC	ACC	AAG	1680
	Leu	Gln	Gly	Gly	Ser	Tyr	Lys	Lys	Ile	Gly	Tyr	Tyr	Asp	Ser	Thr	Lys	
					545					550					555		560
	GAT	GAC	CTT	TCC	TGG	TCT	AAA	ACG	GAC	AAA	TGG	ATT	GTT	ACA	TCC	AGA	1728
40	Asp	Asp	Leu	Ser	Trp	Ser	Lys	Thr	Asp	Lys	Trp	Ile	Val	Thr	Ser	Arg	
					565					570					575		

ACT CCC AGC CCA ACT TGA  
 Thr Pro Ser Pro Thr \*  
 580

1746

5

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 581 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

Met Leu Leu Leu Leu Leu Pro Leu Ala Leu Ala Pro Leu Phe Leu Arg  
 1 5 10 15  
 Pro Pro Gly Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly  
 20 25 30  
 Cys Gln Ile Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly  
 25 35 40 45  
 Leu Thr Arg Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr  
 50 55 60  
 Glu Ile Glu Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys  
 30 65 70 75 80  
 Val Arg Lys Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro  
 85 90 95  
 Ser Arg Cys Val Arg Ile Cys Ser Lys Ser Tyr Leu Ala Leu Glu Asn  
 35 100 105 110  
 Gly Lys Val Phe Leu Thr Gly Gly Asp Leu Pro Ala Leu Asp Gly Ala  
 40 115 120 125  
 Arg Val Asp Phe Arg Cys Asp Pro Asp Phe His Leu Val Gly Ser Ser  
 130 135 140

	Arg Ser Ile Cys Ser Gln Gly Gln Trp Ser Thr Pro Lys Pro His Cys	
	145	150 155 160
5	Gln Val Ser Arg Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly	
	165	170 175
	Ala Leu Phe Pro Met Ser Gly Gly Trp Pro Gly Gly Gln Ala Cys Gln	
	180	185 190
10	Pro Ala Val Glu Met Ala Leu Glu Asp Val Asn Ser Arg Arg Asp Ile	
	195	200 205
	Leu Pro Asp Tyr Glu Leu Lys Leu Ile His His Asp Ser Lys Cys Asp	
15	210	215 220
	Pro Gly Gln Ala Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro	
	225	230 235 240
20	Ile Lys Ile Ile Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val	
	245	250 255
	Ala Glu Ala Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser	
	260	265 270
25	Ser Ser Pro Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg	
	275	280 285
	Thr His Pro Ser Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe	
30	290	295 300
	Glu Lys Trp Gly Trp Arg Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu	
	305	310 315 320
35	Val Phe Thr Ser Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala	
	325	330 335
	Gly Ile Glu Ile Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val	
	340	345 350
40	Pro Val Lys Asn Leu Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu	
	355	360 365



Phe Tyr Glu Thr Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu  
 370 375 380

Arg Leu Phe Gly Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala  
 5 385 390 395 400

Asp Asn Trp Phe Lys Thr Tyr Asp Pro Ser Ile Asn Cys Thr Val Asp  
 405 410 415

10 Glu Met Thr Glu Ala Val Glu Gly His Ile Thr Thr Glu Ile Val Met  
 420 425 430

Leu Asn Pro Ala Asn Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu  
 435 440 445

15 Phe Val Glu Lys Leu Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr  
 450 455 460

Gly Gly Phe Gln Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu  
 20 465 470 475 480

Ala Leu Ala Leu Asn Lys Thr Ser Gly Gly Ser Gly Arg Ser Gly Val  
 485 490 495

25 Arg Leu Glu Asp Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile  
 500 505 510

Tyr Arg Ala Met Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val  
 515 520 525

30 Val Phe Asp Ala Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln  
 530 535 540

Leu Gln Gly Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys  
 35 545 550 555 560

Asp Asp Leu Ser Trp Ser Lys Thr Asp Lys Trp Ile Val Thr Ser Arg  
 565 570 575

40 Thr Pro Ser Pro Thr  
 580

((2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16862 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: exon  
(B) LOCATION:3415..3440

(ix) FEATURE:

- (A) NAME/KEY: intron  
(B) LOCATION:3441..3903

(ix) FEATURE:

- (A) NAME/KEY: exon  
(B) LOCATION:3904..3988

(ix) FEATURE:

- (A) NAME/KEY: intron  
(B) LOCATION:3989..4689

(ix) FEATURE:

- (A) NAME/KEY: exon  
(B) LOCATION:4690..4893

(ix) FEATURE:

- (A) NAME/KEY: intron  
(B) LOCATION:4894..5645

(ix) FEATURE:

- (A) NAME/KEY: exon

(B) LOCATION:5646..5831

(ix) FEATURE:

(A) NAME/KEY: intron

5

(B) LOCATION:5832..7181

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION:7182..7202

10

(ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION:7203..8307

15

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION:8308..8803

(ix) FEATURE:

20

(A) NAME/KEY: intron

(B) LOCATION:8804..12266

(ix) FEATURE:

(A) NAME/KEY: exon

25

(B) LOCATION:12267..12401

(ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION:12402..12815

30

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION:12816..12986

35

(ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION:12987..14085

(ix) FEATURE:

40

(A) NAME/KEY: exon

(B) LOCATION:14086..14187

(ix) FEATURE:

(A) NAME/KEY: intron  
(B) LOCATION:14188..14473

## (ix) FEATURE:

5 (A) NAME/KEY: exon  
(B) LOCATION:14474..14539

## (ix) FEATURE:

10 (A) NAME/KEY: intron  
(B) LOCATION:14540..14998

## (ix) FEATURE:

15 (A) NAME/KEY: exon  
(B) LOCATION:14999..15190

## (ix) FEATURE:

20 (A) NAME/KEY: intron  
(B) LOCATION:15191..16862

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

	GATCATATTA ATTTGAAGGT GCGGGGCGAG GATGGTTCTG TGGTGCAGTT TAAGATTAAG	60
25	AGGCATACAC CACTTAGTAA ACTAATGAAA GCCTATTGTG AACGACAGGG ATTGTCAATG	120
	AGGCAGATCA GATTCCGATT CGACGGGCAA CCAATGAAAC AGACACACCT GCACAGTTGG	180
	AAATGGAGGA TGAAGATACA ATTGATGTGT TCCAACAGCA GACGGGAGGT GTCTACTGAA	240
30	AAGGGAACCT GCTTCTTTAC TCCAGAACTC TGTCTTTTAA AGACCAAGAT TACATTCTCA	300
	ATTAGAAAAC TGCAATTTGC TTCCACCACA TCCTGACTAC TACCGTATAG TTTTCTCTAT	360
35	TCTTTCATTT CCCCTTCCC CATTCCTTTA CTGTACATAA AGTAACTGGT ATATGTGCAC	420
	AAGCATATTA CTTTTTTTTT TTAAACTAA ACAGCCAATG GTATGTTTTG ATTGACATCA	480
	AGTGGAGACG GGGGGGAAAA TACTGATTCT GTGAAAATAC CCCCTTCTC CATTAGTGGC	540
40	ATGCTCATTC AGCTCTTATC TTTATATTCC AGTAAGTTAT TTTGCTCTCA CTGTTTAAAC	600
	AACAACAACA AAAAAACAAC AACATAAAAA TCCTGCATA CCTTGTTCAA TTGGAGAATT	660

	TTAATGTTTT TCATTTATCA TTGTAAAACC AAGGACAATT TTATAACTTT TTTGTACTTA	720
	GCTGTTACAT GCAGAGCAAT CTGTCTTTAA GTAGGGATAA ATTACTCTAA AACAAAAAAG	780
5	AATCCTAGAT AGTTTTCCCT TCAAGTCAAG CGTCTTGTG TTTAAATAAA CTTCTTGT	840
	AAAAAAAAAA AAAGTAAAAA AGAAAAGTTA TGCAACAATT AATGGCCCAG AGGCAATCCT	900
10	TGTTAACATT TTGATGCATC TTTTAGCTGT TTTTTTTTTT TTTTTTTTTT TTGACTGAGT	960
	TTGACTCTTG TCACCCAGGC TGAAGTGCAA TGGCATGGCA TGATCTTGGC TCACTGCAAC	1020
	CTCCGCCTCC CGGGTTCAAG TGATTCTCCT GCCTCAGCCT CCTGAGTAGC TAGGATTACG	1080
15	GGCATGCACC ACCATGCCTG GCTAATTTTG TATTTT TAGT AGAGTTGGGG CTTCTCCACA	1140
	CTGGTCAGGC TGGTCTCGAA CTCCCAACCT CAGGTGATAA GGGAAGGGGC ACTATTGACA	1200
20	TTTATGGTTG GGGCAGAGGT GTAAGATATT CTTCAAAGCA CTACCTACAT GTTGAAGAAT	1260
	TGTTCCCTCAC CCAGATTCTC AAAAGTCCCC CAGGACATTC ACGTAGTGAA AACCTGTGTT	1320
	TAATTATCTG AGCCTATAAC TTAATACAGT TTTAAATTT TTTTTTAAAT ATACAGTGAA	1380
25	CTTTCTAGGA ATGCAATTAT AGTTGTGTGT AAAATTAGGG AAAATTAACT TTGCTACCAA	1440
	GAGTTGTTCA ACATTTTGTT AAATCACTTC ATTGATGGCA ACATGCTGGA GGTAGTTGAG	1500
30	TCACCAACTC AGCACCTGGA TCAGCCTGTG TTGGTAGCAG TTTCATCCCC GTGGTTCTGT	1560
	GAATAGGTGG AAGCATCTGC TTA CTCCATC AGGACTTCTA GGGTAGTCGG GCCTTGGCAC	1620
	TCACACATTA AAATACTGTT TATGTTATTT TATTGCAAGT TACTTTTCTT TCATTTCCCC	1680
35	TTTACGTTAC AGAAAGGGAA GCATTTTGCT TTCTGTTTAA AGTTGTGTAT GTAGGTAGGT	1740
	TATATCATCT AWGACTTTCT CTCCCTCCTT CCCTTTCTTT TTGTTTGAGA TGGAGTCTTG	1800
40	CTCTGTCACC CAGGCTGGAG TGCAGTGGTG CGATCTTGGC TCACTGCAAC CTCTGCCTCC	1860
	CGGGTTCAAG CGATTCTGGT GTCTCAGCTG GGATTACAGG CGCACACCAT CACACCACGC	1920

	TAATTTTCT ATTTTATAGTA GAGATGGGGT TTCGCCATGC TGGCCAGGCC AGGCTGGTCT	1980
	CAAACCTCTG AGCTCAAGTG ATCAGTCCGC CTCGGCCTCC CAAAGTTCTG GGATTTTCAGG	2040
5	CGTGAGCCTC ATCTATGAAT CTCAATTTAG GACAGTAAAA GTGTCATTAC AAAAATATTT	2100
	ATTGTAAAAA AGGGTTGGAG GTTGAGAATC TCAATTCTAG TCAGTCTCTC AGTGTTTGGT	2160
	TTCTTCCTAC CATTTTTCCT CCTAGGACCA GCCAGAAAGC AGCTTTTTTTT TTGTCCCCC	2220
10	CAACAAGGAG CCCACTGTTT CCTCTCCCAG CCCAACTCA GGCCTACGAA CAACAACAGC	2280
	ACTACACACA CACACACACA CACACACACA CACACACACA CACCCCTCCA CTTCAAGGTA	2340
15	TAGCCAAGAG CTTCTGGAGC CGTCAAAAAG GTCTGTACCT GCTGTCTTTA GAGCTTCCAG	2400
	TTTGCCCTTG GTCAAGAAAT ACTGTTTGCT AGGCTCTGCT GGAGTACATC AGGTAATACT	2460
	GGCTTCTAAA CCACCCTGAG GTTCTTTTCT CTTGTCTTTT TACTCCCTTC GTACTTCAAT	2520
20	TTCTCTCCTT GATGTCCCCC TCCCTGTTTT GTTTTTTGCC TCCAATCCGT TCTGCGCGTT	2580
	CCCTGCAGAG CAGGCGAGTA GCAATGCTGC TGGACCATGG AGCTGCTCTA GTCTCCCAGA	2640
25	AATCTCTTCT ACACCCAACC CTTCTTGCGC TTAGGTGGTC CTCAGTCCCC CTCCCCCACC	2700
	TCCTTCTGAC CCAGGCTTCT TTCTCGCCCT CCGGTGCGAG TTCTCCTGGG CATCTGCCTC	2760
	TGCCTCTCTC CTCTCACCCG GATCTAGGGC TGCCTTCTCT TTGTGCAGCC GTCTTTCTCC	2820
30	ACCTTCATCC CAGACTCCCT GTCTCAGCGC CAGCTCCTCT GCCTTTGGCT CGGGTTCCCT	2880
	CTCCCCCACC CCAGCTTCCA GTTGTTTGGC CCGCAGGTCC CTCGGCAGTG ACCGGCGCCC	2940
35	CCCACGAGT GCGTGTGCAC CAGGGCACCT CCTCTCCCC CACCTCTCAG CCCCGCGCCT	3000
	CTCCACCGCC CGCCCCACCG CGCTGTGGGC GGTCCAGGGC GGGGCTGGGA TCCGGGGCGG	3060
	CTCCCGGGGC TCGGGTTGTG GGAGGCGCCC TCTCCCCGGT CTTCCCTCTCT CTTCCCCCG	3120
40	CCCTGCCTTC CCTTGACCCC TCCTTCTTCC CTCCGCCCCG GAGCTCTCCC TGGTCCCCGG	3180
	CGCCGCTTCC TTCCCTCCCC GCTCCCCGCT CCCCCTCCCC GTGGCTGCCG CCGCCCCGGG	3240

	GAAGAAGAGA	CAGGGGTGGG	TTTTGGGGGA	AGCGAGAGAG	GAGGGGAGAG	ACCCTGGCCA	3300
	GGCTGGAGCC	TGGATTCGAG	GGGAGGAGGG	ACGGGAGGAG	GAGAAAGGTG	GAGGAGAAGG	3360
5	GAGGGGGGAG	CGGGGAGGAG	CGGCCGGGCC	TGGGGCCTTG	AGGCCCGGGG	AGAGCCGGGG	3420
	AGCCGGGCCC	GCGCGCCGAG	GTAAGAGCCA	GGGCCCGGGG	TTAGCAGGGC	TCGGAGAGGG	3480
10	GGCGCGCGGC	GTGGTGGGGG	AGGGGGCAGT	GGGCGCAGGG	CCCAGCTGGG	GGAAGCGGGG	3540
	CTGGGGGAGA	GGAGGAACCG	CGGGGATGGA	ATCGGGGAGC	GCTGAGGCGG	CCGATGCCGG	3600
	GAGCGTGGGT	AAGCCAGGCT	TCTGCGAGCC	GCGGGGGCCG	GGGGAGAGGA	GGTGGTGAGA	3660
15	GGTGGAGTCC	GGGAGGGTTG	GGGGCCGAGG	GAGGCAGGAG	GAGGGTGGGG	ACAGGCTTTC	3720
	TCTCCTCCTC	TCCCCCACC	CCGCGCGGGG	CTCCGCCCCC	GCCTCCTCCG	CGGGGCGCTC	3780
20	TCTTGGTCCC	CAGGCTGAGC	CCGGTCGGAG	CCTGCGAGGC	AACCGGCAAG	AGGTCGAGTA	3840
	GTCTCCGGGT	GCGGGCCGCG	CCGGCGGGGC	TCGGTCCAGT	CCTCATGGCC	GCCTCTCACT	3900
	TAGATGTTGC	TGCTGCTGCT	ACTGGCGCCA	CTCTTCCTCC	GCCCCCGGGG	CGCGGGCGGG	3960
25	GCGCAGACCC	CCAACGCCAC	CTCAGAAGGT	GCATCCTTCT	TCGACGACCT	CCGGCCCTCC	4020
	TCGCTCCAC	TTCCCTTTCC	CTGCATCTCC	TCATTTCTGG	TCCTCATCAC	TATCCCATCA	4080
30	GTCCACATA	TCATCCCGGT	CTGGCAACCC	CTTCTGCTCG	GCCCCACTTT	ACTACTGCTG	4140
	ACCTCCTTCT	GTCACCCAC	GTTACTATCC	AGCACCTCTT	TTCTCTGCCC	ACATTGCTAC	4200
	ACTATACCAC	CTTCCTGTGC	ATTTTCTCCG	CCTCAATCCC	CTTCCCAGC	CCCACATTAC	4260
35	TACCTCAATT	ACTCCCTTTT	CTTGGTCCCA	CTTGCTGTG	CAGATGATCT	TATTAGCCTC	4320
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5	CACTGGGGAG	CCTGCCTTTT	CCTCTTTCCC	ACCATTCCTC	TCTGTATGCC	TCCCCGACTC	4680
	ACCCCTTAGG	TTGCCAGATC	ATACACCCGC	CCTGGGAAGG	GGGCATCAGG	TACCGGGGCC	4740
	TGACTCGGGA	CCAGGTGAAG	GCTATCAACT	TCCTGCCAGT	GGACTATGAG	ATTGAGTATG	4800
10	TGTGCCGGGG	GGAGCGCGAG	GTGGTGGGGC	CCAAGGTCCG	CAAGTGCCTG	GCCAACGGCT	4860
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15	CTTCAAGACT	ATTCCTTTTC	CTGCCGAAA	CTTAGCATT	CTGCTTGCAA	GTCAGCACTT	4980
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40	GGGTGGGGAC	CTCCAGCTC	TGGACGGAGC	CCGGGTGGAT	TTCCGGTGTG	ACCCCGACTT	5760
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5	AGGACACTGG	AAAGGGGAGA	TGAAAGTCCC	TTTTCCTCC	ATCACCTGCC	TCAAACCTCC	6000
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30 AGACAGCTGG TTAATGACAG ACTTGAGCG AGGAGGCGCA TTCTCTGATT TGAGAGGGCT 15780

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35 TTCTTTGTG CTCAGCACTA CATTGTAAAG AGTACAGGAA TTTTGGGTAA GCTCGATACG 15900

GCCACCTATG TGTCTGCTTA TTACACCAAG TGTGTACCTG CTTTGAGAG CATGTTAGGG 15960

GTGAGTTAAT GGTGTAAAG CCCCAAATA GCTTGATTTA AAAAGTTTCTA CTAACAGTGG 16020

40 CATTTGTGTG GACTTAGAT TCATGATTTC AGGGATTCTA ACAGCAAAAC TCTGATGTGG 16080

ACTTATCTAC ATTTTGTAGA CCAGGAAAT GAGACTCAGA GTGGTTTAAT GACTTGCTCTC 16140



AGGTCATGCA GCTACTCAGC AGTCCAGCTG GAATTGAATC CTAGTTAAAT CTGGCTCCAA 16200  
ACTGCTCTGC TCATCACTTC CCATGGAAAA CCATGAAGCC TGAATAAAAA GTTTGTACTT 16260  
5 TTATCTGCTA ACACTGTTTA GCTACTGGCA ATTGCTGAGC AAAGGAGAAA TAAGATTTAG 16320  
GAAGTTGACT CTGGTGGTGT GTTGTGATGA AAGATCTGCT GCCACATGGA CTCTGATGAT 16380  
10 ACACACTGTT TTGGGACATT CTAAATGGAC TCTATGTTTT AAGGTATGTT AGTTGAAAAA 16440  
TACAATGAAA AAATTTTGGA AGATCACTTT CCTGTAGAGT ACCCAAGAGG TGAGTCATCC 16500  
ATAAAACCTG GGAAAGTATT GGAAGTGGCT ACCAAAGCCA GAAAGACTTG TTGGTGCCCT 16560  
15 GAGCCCAGGA CTTGCCAATC GTTGCTTCTG TCTTATAGCA GGGAGCTAGA GGAGGCTGAC 16620  
AGAAAACAGG GATTGGCTG GATCTAGTGG CTCACACCTG TAGTCCCCAG CACCTTGGGA 16680  
20 GGCCAAGGCA GAGGATCACT GGAGCCCAGG AGTTCAAGAC CAGCCTGGGC AATATAGTGA 16740  
GACCCCCAGC TCTAAACAAA AAGAGAGAGA GAGAGAACAG AGAGATGGTT AGGGACATAG 16800  
AGGGACACCT GAGCATTTGGG GTGGGAAGAC TTGGAAGGTC CCTTTCTGAC TTTGTGTCTA 16860  
25 GA 16862

30

(2) INFORMATION FOR SEQ ID NO: 61:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16707 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (ii) MOLECULE TYPE: DNA (genomic)

40

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION:1..2742

## (ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION:2743..2985

## (ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION:2986..3613

## (ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION:3614..3677

## (ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION:3678..5226

## (ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION:5227..5304

## (ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION:5305..6848

## (ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION:6849..6999

## (ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION:7000..7494

## (ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION:7495..7627

(B) LOCATION:11370..11591

(ix) FEATURE:

(A) NAME/KEY: exon

5 (B) LOCATION:11592..11735

(ix) FEATURE:

(A) NAME/KEY: intron

10 (B) LOCATION:11736..12512

(ix) FEATURE:

(A) NAME/KEY: exon

15 (B) LOCATION:12513..13999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

AGCTAATTTT	GGAATTTTTT	TTTTTGAGAC	AGAGTTTCAT	TCTTATTGCC	CAGGCTTGAG	60
20	TGCAATGGCG	CGATCTTGGC	TCACAGCAAC	CTCCGCCTCC	CAGGTTC AAG	120
	GCCTCAGCCT	CCGGAGTAGC	TGGGATTACA	GGCATGCGCC	ACCACACCCG	180
	TATTTTTAGT	AGAGACAGGG	TTTCTCCATG	TTGCTCAGGC	TGGTCTCGAA	240
25	CAGGTGATCC	ACCCGCCTCA	GCCTCCCAAA	GTGCTGGGAT	TACAGGCGTG	300
	CCCAGCTAAT	TTTTGTATTT	TTCATAGAGA	CAGGGTTTCA	CCATGTTGGC	360
30	TTGAACTCCT	GACCTCATGA	TCTGCCCCGC	TTGACCTCCC	AAAGTCCTGA	420
	GTGAGCCTCC	GTGCCCAGGC	CAAGTCTGGC	TAATTTTTAA	AAAAATTTTG	480
	TCCTCTCTGT	TTTGCCCAGT	CTTGCTCTCA	ACTCCTGGGC	TCAAGGAATC	540
35	GGCCTCTGAA	AATGAAAATG	TTGGGATTAC	AGGCGTGAGC	CCCCTGTGCC	600
	TTTTTTTTTT	TTTTTTTAAA	GGCAGAGTCT	CACTCCATCG	CCCAGGCTGA	660
40	CGTGATCTCT	GCTCACTGCA	ACCTCTGCCT	CTTGAGTTCA	AGCGATTCTT	720
	TTCCCAAGTA	GCTGGGATTA	CGGGAGCCCA	CCAACACACC	CAGCTAATTT	780

	AGTAGAGACG GGTTCACCA GGTGGCCAG GCTGTCTGGA ATTCCTGACC TCAGGTGATC	840
	CACCCCTCCTT GGCCTCCCAA AGAGCTGGGA TTACAAGTGT GAGCCACTGT GCCCAGCCTG	900
5	ACTTGTTTTT TATAATGCCT TTTTTTTTTT TTTTGTAGAC GGAGTCTTGC TCTGTCGCCC	960
	AGGCTGGAGT GTAGTGGCGT CATCTCAGCT CACTGTAACC TCCACCTCCT GGGTTGAAGT	1020
	GATTTTCTCA CCTCAGCCCT CAGCCTCCTG AGTAGTTGGG ACTGCAAGTG CACACCACCA	1080
10	TGCCCAGCTA ATTTTTTGTA TTTTAGTAGA GATGGGGTTT CACCATGTTG CCCAGCTGGT	1140
	CTTTAACTCC TGAGCTCAGG CAGTCTGCTT ACCTTGGCCT CCCAAAGTGC TAGGATTAAA	1200
15	GGTGTGAGCC ACTGTGCCTG GCCTTTTTTT TTTTTTTTTT TTTTGTGAGC AGTTTGTAGT	1260
	TCCCAGCAGA ATTGAGATGA AGGTACAGAA ACTTCCCATA TGCTTCCCAC ATGCATAGCC	1320
	TTCTACATTA TCGACATCCT CCGCCAGAGT GGTACATTTG TTACAACTGA TGAACCTACA	1380
20	TTGATACATC ATAATCACCC AAAGTCCATA GTTACATTA GAGTTCACCC TTGGTGTAT	1440
	ATATTCTATG GGTGTGGACA AATGTATAAT GAGACGTATC TACTATTAAA TACTTTACAG	1500
25	AGTATTTTCA CTGGCCTAAT CCAATGGACA TTTATTGTGA CTTCAATTATG GTTGGGCACA	1560
	GTGCTAGATG CTGATGATTA AGAGAGGGCA TGGGATTTGG TCTGTCTCTC AAGGGTAGAA	1620
	CCTAGGCCCA TTGCATCTTC AAAGCCCAGG CTCCTTCAAA GCCCAGTGTA GTAGCAACTG	1680
30	CTGTACCTTG CCTGTGCCCT TTGCGTATCT CACTCCTCTA TCTCTCTAGA AAGTTGGAGA	1740
	GAAAAGTGAG CAAGGCATGA GGAACAAAGT TATTATTTA TTCTTCATTC ATCTATTTAT	1800
35	TCTTTCATTA CCGTTTGTGT TAAAACATTC CAAACCCAAA CAATTATTTG TATGGTCCCC	1860
	TGTGTATTAC TTGTGGTTTC CCAAGAAGTA GTTGCTAAGC TTTTCCTTGT ATGGTTTCTG	1920
	TGAGGTAAGG AAGGAATGAT GTGATTTTCT CCAGTATGTA GAATGCAGTT CCAAGAGGTT	1980
40	AAGTAATTTA CTTACAGTTA TTTAGCCAAA CAAGGTTACT GCAAGGTATA TGAAGTCAGG	2040
	TCTCTTGACC CAGTTCATGA GAGAGTTAAA GGAAGTATCA TTCTTTTGTAG CTTTCATGGA	2100

	AAAAGAAGGT TGAGTGTGG GAGGGGTGTG GGTAGGATTG ATAATGGACT TCAAAAATGT	2160
	GAAGGGTATT TCTGTAGTTT TCATTCTTCT GAAAGCCTTC TAAGAGGCAG TGAACCAAAA	2220
5	GCACACAAGA ATGGCAAGAA GTTAGCATGC TGAAGAAATA TCCTCCTGGC TGGCAAGCAG	2280
	AGTGAGAAGA CTGCTATCAC CTTTCTAGA ATCTTTTGA ATTGTAGGAG CTGTTAGATC	2340
10	CTGGGTAAAC TCTATGAAGA AAGTCAGAAG GATCAGAGAA CATCAGTGTC ACAGCTCTTC	2400
	ATTGGAATAT CCATGTCTCC TCCTTTACTC TGCTCTACCT TCCATCCTTT GCCACTAATT	2460
	ATCCAGAGTG TTTGTCAAAA TTCTCTGTTT GCAGTTCTGA GCTAGCAACT GTACACACTA	2520
15	ACACCATCAG ACACAGCTAA TACCTACTCT AGTCTAGTAG CTTCCGATCT AAGGCAGACA	2580
	CATGGGTATA GTTAAAGATT TTGAATGTAC ATGTGTCCAA TCTGACAACA GTAACACAAA	2640
20	CCATCCATTC AAGTAGAAGT GATTGAGTCA GAATTGGATT GCACCCCTTC CCCACACCC	2700
	ACACACATTT CAGTTCTTTC CTCATGATTT TTTCCTCCCA AGACATCCCA GGAATTTGTG	2760
	GAGAAACTAA CCAAGCGACT GAAAAGACAC CCTGAGGAGA CAGGAGGCTT CCAGGAGGCA	2820
25	CCGCTGGCCT ATGATGCCAT CTGGGCCTTG GCACTGGCCC TGAACAAGAC ATCTGGAGGA	2880
	GGCGGCCGTT CTGGTGTGCG CCTGGAGGAC TTCAACTACA ACAACCAGAC CATTACCGAC	2940
30	CAAATCTACC GGGCAATGAA CTCTTCGTCC TTTGAGGGTG TCTCTGTGAG TTAAAACTTC	3000
	CTTCATACTC CCCTGTCTTC CCAATCTTGA GAGAGACTCC CAAGAGGCAC CTTCTACAAA	3060
	CATGCATTCT CTGTTTTTCT CAGTTACTTC TTTGCAGAAT CAGTCTCCGA CCAGAGAAGT	3120
35	AGGGACCTTC AAATTAGAAG AACCCATCAA AGACTAGAGG AAAAAAATG ATGTATTCCA	3180
	TTTTTTTAAA CCCCTCCCCT CATTTCTTTT CAACTAGAC CAAGTATTCA TGAGTCAGAT	3240
40	GAGAACTATA GGATTTTGAA AGACAAAACA GTCTGAAAGG TCATCTTCTT ATTCCTTTTA	3300
	AAATGAAAAG ATTAGTTTCC AGAGAGATTT GCTGACTTGC TTAGGCCACA CAACCAGAAG	3360

	CCTGCTGGTG	TTCTGTCTGG	GGATTTTTTC	CCATTCAAAT	CTCATAAGTG	AAGCTCCTTC	3420
	TCCAAAGAAT	AATGTTTCTA	AAATCTAGGG	TATGGGCATC	TGGGGTATGT	CCTATATGCA	3480
5	GGCAAATGCC	ATAAATAGCA	TTCATTGAGA	GGCTCAATTA	CATCAAAAAC	AGAAGGATTT	3540
	AAAGAGTCCC	TGATGTTCTC	TTTCACTCTT	GCTTTTGTCT	CCTTTGCCTT	GCTCCACATG	3600
	TTCTTCCCT	CAGGGCCATG	TGGTGTGTTGA	TGCCAGCGGC	TCTCGGATGG	CATGGACGCT	3660
10	TATCGAGCAG	CTTCAGGGTT	AGTACAGGGG	CAGGAGGGGA	CCGGACATGG	GGGCTAGGCT	3720
	GGGGCTGGGC	TGGGATGCCC	CCTGGGGAAG	AATGCCAGAG	ACATCACAAG	ATTGCCCTGG	3780
15	CACCTCCCAA	CTTCTGCCCT	TCTCTTTTAA	CTCTGTTTAT	CAAGCTTGTA	AATAATAATA	3840
	ATAATAAGCT	TAATAACAAG	AAGATTGATG	TCTTTGAGTT	GCACTGGTTT	TGCTCTTGAA	3900
	AAGAGGTGTG	CAGGCTGGGT	GTGGTGGCTC	ACCCCTGTAA	TCCCAGCACT	TTTGGGAGGC	3960
20	CAAGGCAGGC	AGATCATGAT	CATGGTCAGG	AGTTTGAGAC	CAGCCAGACC	AACATGGTGA	4020
	AACCTGTCTC	TACCAAAAAT	ACAAAAAATA	AAAAAAAAT	TAGCTGGGTG	TGGTGGCAGG	4080
25	TGCCTGTAGT	CCCAGCTACT	TGGGAGGCTG	AGGCAGGAGA	ATCACTTGAA	CCCAGGAGGC	4140
	AGAGGTGCA	GTGAGCTGAG	ATCACGCCAC	TGCACTCCAG	CCTGGGTGAT	AGAGTAAGAC	4200
	TCTGTCTCAA	AGAAAAAAGA	AAAGAAAAGA	GACATGCAAA	TTAAAAACAG	CTACTCTCTT	4260
30	TCCCAGTGGC	TTCCATTAAAT	TTCAGGAATT	TCCCCTTGAG	TGGCTTGGGT	TGAGAGGTTG	4320
	ATGACCTGTC	AGTTAGACTC	AAGAAAGCTG	AATCTAGGAG	AACCGCTATT	TTTTTTTTTAA	4380
35	GGGAATCTGC	CAAATTTCCCT	TGCTGTGTAA	AGCTTCAATG	TGTATAGCTT	GGCTTTTGTA	4440
	GATTGTATTT	TCTTGAAACT	TAGCACACAG	GTATTGTCAG	AACTTCTAGG	AGTTAATTTT	4500
	TCTGCTCCAC	TCGGCTCTCA	GTCTTTTACG	GCATGGCCAA	GAGAGCTATT	TCTTGGCCTC	4560
40	CTGTGAAAAG	TTTCTTTCTT	CCTTTCTCCC	CACCTCCACA	TCCTTTCAGC	TCCTCTTTGT	4620
	ATCCAGGACA	AGAGGAAATG	GACTTCAGCC	ATGGTGAAAG	GAGTGTGAGT	TGGCTTTTGA	4680

	AGGAAAAGTT ATGGTAACGG AAACAGTTCT AGAACAGAAA TCTTAGAAAT GACCAAATTT	4740
	TACTCAATGG CGCTTTAAGA GGCAGATATA ACTTATCCAA GGAATTAAAA CCAAGCCAA	4800
5	CAGAAGAGAA TGTCTAAAA TTAATGAA AGCCACTGGG AAAATAGAGC CTGCCCATCA	4860
	TGAGAGGAAG AATAAGCAGA AATATGTGTA AAGCTTTAGA AGCCAAAATC AAAGTGAGAG	4920
10	ACATCTCGCC GAGAGAGGTG TGAGGAATGG AATAGGTGGC AGACATGTTG TGGAGCCTCC	4980
	TCCTGAAGA CTTTAAACA TAGATATTCT TATTTATTTG AGTTGTCTTG GGAACCACCT	5040
	TATATTGCTT TTAAGTCATG TTGCTGATTC AAGAGTCTCG TAGGTCCTTC CAAGCATCCT	5100
15	TAGGGCCTCA GGTGAAAATA AAATCAGATA CAACCATGCA AAGCTCTAGG GAAGTGGGAA	5160
	GTTGAAAATG CCTAGGATCA GCTCTTTGGC TACCTGTGGT CACTCCTTTT ATTGTCTCT	5220
20	GCCCAGGTGG CAGCTACAAG AAGATTGGCT ACTATGACAG CACCAAGGAT GATCTTTCCT	5280
	GGTCCAAAAC AGATAAATGG ATTGGTGAGT GGATCTTGTT TGTATTTTCC TTCAGCCCCT	5340
	CTCGACAGTC AAGGGAAAAA GTCATGCCTT TGAGTGAGGA TGAATGGTA GAGACTGTTA	5400
25	GGTTGGAATG TGGCTGGCAG CTGGGCCAGG AGAAAGGGT AAGTGAGAGT GAATACAACC	5460
	CCTAAGGCGT GGGTAGGGGA GACTGGTGTA TTTGGAGAGG GAATAGGCGG TGGTTAGTAC	5520
30	TATTTTAAAT GGTGCATTGC TGGGGTAACT GGGGATTAGA GGCAGGGGGT GGCAGAGGG	5580
	CGGGAAATGG AACTCCATT TGGGTTTCCC AGATGTCCTG GTGCTTGAT ATATTTGAAC	5640
	CAGCTACTTC AAGCCCAGAG CTGTCTCTTT GTCTGTCTCT GTCAGGAAAA CGGTTGCTTA	5700
35	AACTATGGAG GAGGAGGGAA AACCTCATGT AATTGTCATC TGCCAAAATG TGCTTTTAT	5760
	TTTTATATGT ATTTTAAAA ATTTTCCTAT TTTTATGTAA TTTAGAGGTA GACGTGCAGT	5820
40	TGTGTTACAT GAATATATTG CATAGTGGTG AAGTCCGGGC GTTAGTGTG CCTGTCACCC	5880
	GAACAGTGCA CCTGTACCT AATAGGTAGT ATTACATCCC TCAAAATATA CTTTTTAAAG	5940

	AGAGAAAGCA AGCAGTTATT CTTTGTGTAC TTGGTCTAAA TGATAGGACA TAGGAGAGAA	6000
	ACTGAAGGTG GACAAAAGGA AGGACCTACT GATAAAAGAA AGCCTCCTTG AGAATGAAGG	6060
5	GGAGGCTCAA CCATTGAAGA TGGCTGCCGT CTGCCCTGCC CAGCAGATAT CCAGTCATTC	6120
	CCAGCACTGC TGGAGTTTTG CCCTTTTTTT TTTTTTTTTT CAATTCGAAT TTAGGACAAT	6180
	GTTCTGGATT GCTATAAATG CTGCATGGCC TAAATTATTC TTAAAAAAA AACTAAGCA	6240
10	AATTGAAATT AGTTTTTTTT GGTGAACTCT GACAAATTG AACTTCCCC TAATAATAAC	6300
	TGGAACAT ATTTGGGAAT ATTACCCTGC CAGGATTAAA ATTCAGATT AGCTTTCCTT	6360
15	CTTTTTTGT TTGTCTTAAG AATAGGTGTC CACACTAGAT ACTTCAAGGC CTTTTTAGCT	6420
	TTATGATTCC ATAATTGTCA TTAAAACTT TGATTTGGGT TATAAGAAAC CTTATAACAT	6480
	TTTTTAATGA TCCCCTTCTT TCTCCTCCCA TTTCCTTTG CTGTAAGAA GACAGAAAA	6540
20	CTTAAAGAAC AAACAAAAAC AAAGACTACA ACTTTGGGA CATGCCTCAG CATTTCCCAA	6600
	CCTATGGATA GACCATTAC TCCATCTTCT CATCTCATTT CTGGTTGCTT CCTAACGGCC	6660
25	CCAGTGGCAC TGAGCATTCT GCCTGCAGTA ACCTCTGTCC AGTGCAGTTA GGGCCTCATG	6720
	TCCCCAGCCA ATGACTGAAT GTCCATCAGC AATCTAGTTC TTGCCCCTT TCTCCTATCC	6780
	CGTCTTCATT CCTTTGTCTT CCTTCCCTTC TCTTTTCCCT TCCCCTCTTC CTCCCCTGTG	6840
30	CCATGCAGGA GGGTCCCCC CAGCTGACCA GACCCTGGTC ATCAAGACAT TCCGCTTCTT	6900
	GTCACAGAAA CTCTTTATCT CCGTCTCAGT TCTCTCCAGC CTGGGCATTG TCCTAGCTGT	6960
35	TGTCTGTCTG TCCTTTAACA TCTACAACTC ACATGTCCGG TAAGTTTCTC TTCTGACGTT	7020
	TTCCTTGTCT GCCTCTCTGA GATACTGATC ATGTTCTGG ACAGGATGAG AATAAACCT	7080
	GTGTAACTCC CATGGCCATG TATCATGGAG TTTTTCATTC TGAATTGTTG AGAATGAAAA	7140
40	CAGGGAAACC AGATATAACC CCCACTCCTA CTCCAAAGTA GCTAACGGGA GGAAAAAAGA	7200
	AAAGAAGAGA AAAAAACAAC CTTTGGGGCC AGGTCTCACA GTCTTGACT CTACATAAAT	7260



	AGCCTGTATT CTAGTGGGGG CCTGTGCTTG GGAAGCCCTC TGCAACTCCA TCTTCAGCCC	7320
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5	AGCCCCCTGGC CCTGAAATTA GGGTCATGCC ATTGCGTGGT ATTTGGAGAG CTCAGCCTCC	7440
	CTGGAGAAGA GGGGTAATTC TCTCTCCCTC TCACCCTCTC CACCTCTGCC CTAGTTATAT	7500
10	CCAGAACTCA CAGCCCAACC TGAACAACCT GACTGCTGTG GGCTGCTCAC TGGCTTTAGC	7560
	TGCTGTCTTC CCCCTGGGGC TCGATGGTTA CCACATTGGG AGGAACCAGT TTCCTTTCGT	7620
	CTGCCAGGTG AGGAGGTGGT GGGCAAATTC CTTACAGGAT GTGACTCTCC CACCCGTCTC	7680
15	AGGAGCACCT TCCATGATTT ATGATTCTCT GCCCTTCCTC CTCAGCTTTC CCTGACTCTT	7740
	GTCCCTGTTC TTTCTTCTA GCATCACCCC TCTGTCTCTT GTTTGGCTCT GTCCCTTCTT	7800
20	TCTGTGTCTG CAGGCCATTT TCATTCTGTA GTTTACTTGT CAGTTCCAAG GTTGCCATGG	7860
	CAGSCCTYGC AGAGAAGAGG AGGGAGCCAT TGAAGGCAAA GGAAGGGGAT CTGCTCAAAG	7920
	GTCTCCTGAA CAATGGTGGC TTGTCTGTGG TATGGGGGCT GAGAATCAGA ACTGTGGACT	7980
25	TTTTTTGGGA GCCTTTGTTG GGTTTGAAG GATAGAAGCA GAGATGGAAA CACAGCAGAG	8040
	AGTTGGGGGG AAGGGACCAC TGCCACACAG GGGAGGAGGG GCTCTGGGAC TGTGGGTACA	8100
30	TGGAAGGTTT TAGTGCTGTG GGGAGAGGCC AGCTTCAACA GTGATAGTTG AGTGGTTCTC	8160
	TTTTCCACTG GTGGAAACAC CCACTCTTTC TCCTGATCTG CCTGCCTGTC CTTGCTCTCT	8220
	CTTTTTCCTC TGCTCTGTGC TGTCTGATC ATACATCTGT GCACATGGCA TTTCCATGCA	8280
35	CATGCACATG CAGTTCATCA GGAATCCTCT GTTCCCAGTG AGGCCAGAGT GCAGCTGGAG	8340
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40	GCTTTGGGGG CAAAGAAGGG AACACAGTTC ACTGCTGGCG TGATTGGGTG GACCTCACTG	8460
	AAGAGGTGGC ATTTGAATAC TGAAGGACAA ATAGGATTTT ATCAGCTAGA GAAATAGAGG	8520

	AAGGCTACTT CAGGGGCATA GGGAGCATCG TGTGGCTAGA AAATACATGA AAGAGAGTAG	8580
	ATGAAGAGAA AGTGAGTAGT TCAGCATGGC TGGAGCGTGG GGTAGGTGTG GGGCTGGGAG	8640
5	ATGAGCCTAG CTGGACAGGT GGATGGGAGC ATGTTGTGAA GGGTCTGTGT CATATCCAGA	8700
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10	TGTTCAAGGT GGGGAGACTG CTCTCCTCCT GCCGCTCCCC GTCCTGCTCA CATTTTCGCA	8880
	TCCTCCCTGT GCCACCATGA GCTCCCTGCC CGTGCTCCCT GCCCACTCTC CCTTAGGGTT	8940
15	CTGCCCATCC TTAGTGAGT CCCGGCTACT ACTCTACCCT GTTCTGCCTG TGCCCTCTCT	9000
	TCCTTTCTAG GCCCGCCTCT GGCTCCTGGG CCTGGGCTTT AGTCTGGGCT ACGGTTCCAT	9060
	GTTACCAAG ATTTGGTGGG TCCACACGGT CTTACAAAAG AAGGAAGAAA AGAAGGAGTG	9120
20	GAGGAAGGTG AGCTGCTGCC CAATCCTCAG CCCCARATC CTTGGCTCCT GGGGCACAGA	9180
	GCATTTTCCC CTGACGTGCC TGTTCTCCCC ACATATTTAT CCAGACTCTG GAACCCTGGA	9240
25	AGCTGTATGC CACAGTGGGC CTGCTGGTGG GCATGGATGT CCTCACTCTC GCCATCTGGC	9300
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30	TGAAGCTACT TGGAGAGAGT GCCTTCCTCG TATTGGAAGC TCTTCCTTTC CTTCCTAGAA	9480
	GGAGCCCCTC ATAGGCCTCC AGATTCAGCT GAAGAAAGGA AGGGGTGGGA ATCTGGGAAG	9540
35	GGTGTGTAGA ACTTCAGGC ATCAGGGAAA GTGGGGAACA AGCACCTCCA AGGGTTCAGG	9600
	AAAACATTCT TAGGCCTAGA ATGAGATTTG GCATCAGCAT TGAGGGTCTC ATAGGAAAAC	9660
	AGTTGGAAGC CAGAGACTGA GAAGCGTTGA GGAGAGGAGG GGAGGCTGGC AACCATCTTT	9720
40	CTTGTGACCT TGTTTCTGCC CTAGACATTT GCCAAGGAGG AACCTAAGGA AGATATTGAC	9780
	GTCTCTATTC TGCCCCAGCT GGAGCATTGC AGCTCCAGGA AGATGAATAC ATGGCTTGGT	9840

GTGTGGGATG TGGGCAAAGG AGGGCAGGGA TGCACAAAGG CAGGAGGGAA GGCAGGGGTA 9900

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5 GAACACCCTA CTCTTTGTTA TTGCACTAAT CTTTCTGAG AATAGGGGAG AGTTGCTCTT 10020

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10 CAGAGGAACA AGTGGGGGTA ACCCCACCTC CAGACTTGAC ATTATCTTTT AGATCCCCCT 10140

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20 CACAGGGTGA GGTTCGCTAG GTCAGAGGGG TTGGATTGGA GAGGAGGGCC CCCTTTCCAT 10440

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25 TGCTGCTGCT GGAATCTTC CTTGCTTATG AGACCAAGAG TGTGTCCACT GAGAAGATCA 10620

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30 CATTGACCCT GTAGGCTGAC CACAGCAGCC CAGATATAGA GGA CTAGGAA GAATCAATGC 10740

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35 AGTGAAGTAG ATATTAGTAT CCCCACTTTA TAGGTGAGGA AACAGAAACA CAGAGACGTT 10920

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40 TCTGGAGGAC CCGGAATCTG TGCATAGAGA TCCTGGGAGT TCCTGCCTTG AGGGGAGGGG 11040

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 5 CAATGTGTCT TTCCCTCTAG GTCCTGTGCC TCATCACTGC TCCTGTCACC ATGATTCTGT 11280  
 CCAGCCAGCA GGATGCAGCC TTTGCCCTTG CCTCTCTTGC CATAGTTTTC TCCTCCTATA 11340  
 TCACTCTTGT TGTGCTCTTT GTGCCCAAGG TAAGGATCTG GCTTTTCTCC CACCCTCTTT 11400  
 10 GTTCCCATGT TCCCTCCATC CCTCCTTCCT ATATTACTGA GTTCCTCTGC CCTTCCGTTT 11460  
 ACCCTCCTCT CACTCCTCCC CTTGTTTTGG GCCCAACTCT TATCAGCATT CCTTCCACCT 11520  
 15 CCAACCTTCC ATCAGCCAGT CACTAGTACA GTCCTTGCTG GGCCACCCCA CGCCCAAACA 11580  
 TTTGCCCCCA GATGCGCAGG CTGATCACCC GAGGGGAATG GCAGTCGGAG GCGCAGGACA 11640  
 CCATGAAGAC AGGGTCATCG ACCAACAACA ACGAGGAGGA GAAGTCCCGG CTGTTGGAGA 11700  
 20 AGGAGAACCG TGAAGTGGAA AAGATCATTG CTGAGGTGCG GGGGTGGGTG TCAGGGTAGG 11760  
 GTGTTGGAGT GGTCCAGGAG GCTTGCCTCT TAGCTTGGGT TGTCTGAAGC CAAGCCTGAG 11820  
 25 ATACAGGGTC AGATGTTCTT GGCTCATGGA GGGAGGGTCC TAGGAGACAA CCTGTAAGGA 11880  
 GTGAATGGAG CAGCATAGGG GAGGGGAAAG GGCTGAGCAA GATTCTATCT CAGGCAAAAT 11940  
 CCAGTGTGAG CCTGGCAGGT GGAAGGGCTC TGGAGTGGGA GCTATGTGGT TGAATCAGCC 12000  
 30 TCCTTAAGGC AAGAGGATGG CTGTTGGCTG TAGGTGACAA CTGGAGAGAG GCAGCTGTGA 12060  
 GCCTCTAGTA GTCAACACTC ACAGCAGCTG GGCTAGCAT GCAGCCCCAG CATAAAGGAC 12120  
 35 CTGGGCAGGC GTTCACTGTG CCCCAGGCTG TCATTAGGGG CTGGTGCAAT GCCAAAGAGA 12180  
 GGGATGTTCC AACTGGGTTG ACACATCTCT CTGATTTATT GGAAGCTCTG TGCACTGACT 12240  
 TTTCTCTCCT TCCCCACTTT TTCCTTTTGT TTTTAAATTC TCTCTTATTT CCCTGATCGC 12300  
 40 ATTTTTTCTA TCGGTATCCT TATGTTCTCT GGCTTTTCTT GTTCTGTTTT GATTTCTCCT 12360  
 TTTAATTTAT TCTGTCCACT TACCCTACGT CCTCCCCCTA CATTTTCTG TGCCCTTCCT 12420

	CTCTTTCCCT	GTGCCCTTCC	TCTCTTTCCC	TCCTCCCCAC	TCCTTCATCA	CCTCCTCTTC	12480
	TCCTACTATC	CCAATTGTGC	TTCTTCCTCC	AGAAAGAGGA	GCGTGTCTCT	GAAGTGCGCC	12540
5	ATCAACTCCA	GTCTCGGCAG	CAGCTCCGCT	CCCGGCGCCA	CCCACCGACA	CCCCCAGAAC	12600
	CCTCTGGGGG	CCTGCCCAGG	GGACCCCCTG	AGCCCCCGA	CCGGCTTAGC	TGTGATGGGA	12660
10	GTCGAGTGCA	TTTGCTTTAT	AAGTGAGGGT	AGGGTGAGGG	AGGACAGGCC	AGTAGGGGGA	12720
	GGGAAAGGGA	GAGGGGAAGG	GCAGGGGACT	CAGGAAGCAG	GGGGTCCCCA	TCCCCAGCTG	12780
	GGAAGAACAT	GCTATCCAAT	CTCATCTCTT	GTAAATACAT	GTCCCCCTGT	GAGTTCCTGGG	12840
15	CTGATTTGGG	TCTCTCATAC	CTCTGGGAAA	CAGACCTTTT	TCTCTCTTAC	TGCTTCATGT	12900
	AATTTTGTAT	CACCTCTTCA	CAATTTAGTT	CGTACCTGGC	TTGAAGCTGC	TCACTGCTCA	12960
20	CACGCTGCCT	CCTCAGCAGC	CTCACTGCAT	CTTCTCTTTC	CCATGCAACA	CCCTCTTCTA	13020
	GTTACCACGG	CAACCCCTGC	AGCTCCTCTG	CCTTTGTGCT	CTGTTCTCTGT	CCAGCAGGGG	13080
	TCTCCCAACA	AGTGCTCTTT	CCACCCCAAA	GGGGCCTCTC	CTTTTCTCCA	CTGTCATAAT	13140
25	CTCTTTCCAT	CTTACTTGCC	CTTCTATACT	TTCTCACATG	TGGCTCCCCC	TGAATTTTGC	13200
	TTCTTTGGG	AGCTCATTCT	TTTCGCCAAG	GCTCACATGC	TCCTTGCCCTC	TGCTCTGTGC	13260
30	ACTCACGCTC	AGCACACATG	CATCCTCCCC	TCTCCTGCGT	GTGCCCACTG	AACATGCTCA	13320
	TGTGTACACA	CGCTTTTCCC	GTATGCTTTC	TTCATGTTCA	GTCACATGTG	CTCTCGGGTG	13380
	CCCTGCATTC	ACAGCTACGT	GTGCCCCCTC	CATGGTCATG	GGTCTGCCCT	TGAGCGTGTT	13440
35	TGGGTAGGCA	TGTGCAATTT	GTCTAGCATG	CTGAGTCATG	TCTTTCCCTAT	TTGCACACGT	13500
	CCATGTTTAT	CCATGTACTT	TCCCTGTGTA	CCCTCCATGT	ACCTTGTTGA	CTTCTTCCCC	13560
40	TTAAATCATG	GTATTCTTCT	GACAGAGCCA	TATGTACCCT	ACCCTGCACA	TTGTTATGCA	13620
	CTTTTCCCCA	ATTCATGTTT	GGTGGGGCCA	TCCACACCCT	CTCCTTGTC	CAGAATCTCC	13680

ATTCTGCTC AGATTCCCC CATCTCCATT GCATTCATGT ACTACCCTCA GTCTACACTC 13740  
ACAATCATCT TCTCCCAAGA CTGCTCCCTT TTGTTTTGTG TTTTTTTGAG GGAATTAAG 13800  
5 GAAAAATAAG TGGGGGCAGG TTTGGAGAGC TGCTTCCAGT GGATAGTTGA TGAGAATCCT 13860  
GACCAAAGGA AGGCACCCTT GACTGTTGGG ATAGACAGAT GGACCTATGG GGTGGGAGGT 13920  
GGTGTCCCTT TCACACTGTG GTGTCTCTTG GGAAGGATC TCCCCGAATC TCAATAAACC 13980  
10 AGTGAACAGT GTGACTCGGC ACCTTGCACT CTTCTCTGTA ACAGAATGGG CTTCAATCCA 14040  
AGAAGGGAGG CTCAGAGGAC TCCAAGTTCA TGAAAAGGCA TTAAAGCGGA GGGTGAAAAG 14100  
15 AGGTGTTTTA TTGATCCATT GAGGGCTTAG CAGAATGAAG CAGGACATGA TTAAGTCTGA 14160  
GATTAGTGAG TGAGGACACT ACTGGTTAAA AGTGTGGGCT CTGGAGTCAG ACTGCCAGGG 14220  
TATCAGATCC AACCACATGC AACATTTTC TTAGTCTCTA TTCCCCATGT CCTCATTAT 14280  
20 GAAAATGAGA ATAACAGTAA TACATTCCTC CATAGGTGG GTACAAAGAC TATTATAAAT 14340  
TGTGCATTCA GGTGCCTAGG TTGGCCCTTG GGCCATGGTA TATGTTGCGT GAATGTTAGC 14400  
25 CTCTGTCCCT GCTGTTTAAAT GAGTTCCTTG ACAGTAGTGG GCATGTATTG GGAGCCTGGA 14460  
GCAAGTGCCT AAGCATCCCC TCTAGGGACG CTCCTTCCCA GGAAC TAAGA AGAGTAAAAG 14520  
AATGATGACT GCTAGAAGGT AATGGATGAG ATGGCTGCTG AGTGCTTCCA ACCTTAAACA 14580  
30 TCTTTGTTTA GGAACCTCTGA GCATCTTGGA AATAATTTGC TATCAAACCTG AAAAAAATC 14640  
TTGAATGGAC AAGGGCAAAA ACATTTGCCT GAGACTTTAA ACATTTTTTG TGTCATCTTG 14700  
35 GAGAGTGCTT TTTTGAAGCT CAAATTTTCT TTTATTTTGG CACTGATTTT TAAAGTGATT 14760  
CTCAGATTTT TGTAAGACAG CTGCAAGGGT TGGATGGGCC CTGTCAATCA CTGACCTGTT 14820  
AAGAGCCAAT TTCTGAACTT CCACTAAAGC ATGGGCTGGT TGAATCTTAG ACCAGTACTT 14880  
40 GAAAAACTTT CCACTGTGAT TATCCACCTT GGACCAGTTG GACTTAATTT GAGTCTCTCT 14940  
TCTTCCCACA GTGAAATATC CGCTAGGAAA AGAGAAGAAG TCTATGGAGT AGATAAGCCT 15000

	GCAGTTTGA	AAATGAATAG	TTGGCATCAG	AACAGCAGCA	GGAGGCTGGG	TGTGGTGGCT	15060
	CACGCCTGTA	ATCCCAGCAC	TTTGGGAGGC	TGAGGTGGGT	GGATCACGAG	GTCAGGAGTT	15120
5	CAAGACCAGC	CTGGCCAAGA	TGGCGAAACC	CTGTCTCTAC	TAAAAATACA	AAAATTAGCT	15180
	GGGCGTGATG	GTGGGTGCCT	GTAATCTCAG	CTACTCGGGA	GGCTGAGGCA	GATAATTGCT	15240
10	TGAACCCAGG	AGATGAAGGT	TGCAGTGAGT	TTGTGCCACT	GCACTCCAGC	CTGGGCGACA	15300
	GAGTGAGACT	GTCTCAAAAA	AAAAAAAAAA	GAAAAAAAAA	AAAGAAACAA	CAGTAGCAGG	15360
	AGCTATAGAA	CAGCCCTGGG	TAGAACCTAA	AAGACCCAAA	TTATCATCTC	AAACTTGTCAT	15420
15	TGCACTTAAG	TGGGCTGTAA	ATTATAAACA	AAGGGTGAAA	AGTTCTACTG	TGGCCAAAGG	15480
	TAAGCCAGAC	ACTCTGCTAG	CAGGAGTGCA	GGAGTCGAGA	GCCAAACGGT	GCGGCTAGCA	15540
20	GAGTGCCAG	TGCAAAGGGG	TGGGAAGGAG	TGAGATTGAG	AATATTAAAA	AGGTACTTAG	15600
	AAGAGAACTT	GTAAGATTTT	TACTGGCCAA	ATTTAAAACA	TGACTGAGCA	CTATTTTTC	15660
	TACAGGCCTC	CTACTAATAA	GAAAACAATT	TTGAGATAAC	TACTTATTTG	AGTTCACAGT	15720
25	TAATGTTCTC	GATGATTAAG	ATCAGTTGCA	AATGTTTCATC	TGTCAATGCT	TATCTACAAT	15780
	GAGACTTCAT	GTATTCATTT	CTGAAAGTGT	CTTTTCAGGG	TGAATGGTGC	TATTGATTAG	15840
30	CACTAATACT	AATTATTAGT	ACATTATATA	TAATTACAAT	GAGATATACA	CACACATACA	15900
	CACACACATA	TATACATATA	CACACACACA	ATGATATATA	ATTAATATAT	AATTGTACCC	15960
	CAAGGGGTGC	AAAGGAGATG	TGTTGCCAGG	TGGAGAGGCT	ACCGCTTGGC	AGTTCTGGGA	16020
35	GGACTTGCTC	CCTGTGCACT	GTGAGGCAGG	CTTTGCCTTT	CAGACCTGCC	TTTGGGTAGG	16080
	GTTGAGATCA	CTTTCTAACT	CTGGAATGTC	CTAGAATGTA	GACTGCCTGC	AGGC'TTCCAT	16140
40	GTCCCCTGCT	TTTCCCTGAC	TTAGCCTGTT	GCCTCCCTGC	CCTCCTGTTG	GTTGTCTACC	16200
	AGTAGAGAGC	ACTTTGTGTG	CACTTGGCTG	CTACATTAGT	TAGGTGATCT	TCAACAAGTG	16260

TTGATGGTGA GTTGCTGTGG CAGGTGCTTT TTTTGGCACT GAGGCAAAAT GGTGAGTAAG 16320  
ATGGCTTTCA AGCGTTGTAC CTTCTCGACG TGGGAAGATG ACCAGTAAGC AGAAAAACAA 16380  
5 ACGAGATCAC TTAAGAGAGC AACCAGGAGT GTTGGGCATC TCACAGCCAT TAGCTCTGGT 16440  
GTGAAGGACA AATCTAAAAG CAAGGGGACT GTGTGTTTCAT TTTCTGGGGT CACAAAATA 16500  
AGGAGCAAAG CCAGTATTCA AACTGCATAT ATTATTATCT ATTGCCACAA AACCTGTTAC 16560  
10 CCTAAATGGC TTCAGACAAC AATAATCATT TATTATCCAT CATGGTTTTT GTGGGCTAGA 16620  
AATTCAGATA GGGTACAGTG GGGAGGGTTC ACCCTGCTCC ACAGCATCTG GAAGATCTGA 16680  
15 AGTCTGAGGG TTGTTGTCCA AAAGATC 16707

## 20 (2) INFORMATION FOR SEQ ID NO: 62:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
25 (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

ATGCGCGCCG GCAGCCAACA TGCTGCTGCT GCTGCTGGTG CCTCTCTTCC 50

## (2) INFORMATION FOR SEQ ID NO: 63:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
40 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

GGTCATCCAG CGTTGAGGTG AAGAC

25

5

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

GAAGGTTGCC AGATTATACA TCCGC

25

20

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

CCACGATGAT TCGAGCATCT TGACG

25

35

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

5

CTGGTTCCTC CCAATGTG

18

(2) INFORMATION FOR SEQ ID NO: 67:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

15

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

20

CCAGTGGACT ATGAGATTGA G

21

(2) INFORMATION FOR SEQ ID NO: 68:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

30

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

35

CTGGTTCCTC CCAATGTG

18

(2) INFORMATION FOR SEQ ID NO: 69:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

CCAGTGGACT ATGAGATTGA G

21

10

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2700 base pairs

15

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

20

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

25

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

30

(B) LOCATION:1..2700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

ATG TTG CTG CTG CTG CTA CTG GCG CCA CTC TTC CTC CGC CCC CCG GGC

48

35 Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly

1

5

10

15

GCG GGC GGG GCG CAG ACC CCC AAC GCC ACC TCA GAA GGT TGC CAG ATC

96

Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile

40

20

25

30

ATA CAC CCG CCC TGG GAA GGG GGC ATC AGG TAC CGG GGC CTG ACT CGG

144

Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg

	35	40	45	
	GAC CAG GTG AAG GCT ATC AAC TTC CTG CCA GTG GAC TAT GAG ATT GAG	192		
	Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu			
5	50	55	60	
	TAT GTG TGC CGG GGG GAG CGC GAG GTG GTG GGG CCC AAG GTC CGC AAG	240		
	Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys			
	65	70	75	80
10	TGC CTG GCC AAC GGC TCC TGG ACA GAT ATG GAC ACA CCC AGC CGC TGT	288		
	Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys			
	85	90	95	
15	GTG AAT CGA ACG CCA CAC TCA GAA CGG CGC GCA GTG TAC ATC GGG GCA	336		
	Val Asn Arg Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly Ala			
	100	105	110	
	CTG TTT CCC ATG AGC GGG GGC TGG CCA GGG GGC CAG GCC TGC CAG CCC	384		
20	Leu Phe Pro Met Ser Gly Gly Trp Pro Gly Gly Gln Ala Cys Gln Pro			
	115	120	125	
	GCG GTG GAG ATG GCG CTG GAG GAC GTG AAT AGC CGC AGG GAC ATC CTG	432		
	Ala Val Glu Met Ala Leu Glu Asp Val Asn Ser Arg Arg Asp Ile Leu			
25	130	135	140	
	CCG GAC TAT GAG CTC AAG CTC ATC CAC CAC GAC AGC AAG TGT GAT CCA	480		
	Pro Asp Tyr Glu Leu Lys Leu Ile His His Asp Ser Lys Cys Asp Pro			
	145	150	155	160
30	GGC CAA GCC ACC AAG TAC CTA TAT GAG CTG CTC TAC AAC GAC CCT ATC	528		
	Gly Gln Ala Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro Ile			
	165	170	175	
35	AAG ATC ATC CTT ATG CCT GGC TGC AGC TCT GTC TCC ACG CTG GTG GCT	576		
	Lys Ile Ile Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val Ala			
	180	185	190	
	GAG GCT GCT AGG ATG TGG AAC CTC ATT GTG CTT TCC TAT GGC TCC AGC	624		
40	Glu Ala Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser Ser			
	195	200	205	
	TCA CCA GCC CTG TCA AAC CGG CAG CGT TTC CCC ACT TTC TTC CGA ACG	672		

	Ser	Pro	Ala	Leu	Ser	Asn	Arg	Gln	Arg	Phe	Pro	Thr	Phe	Phe	Arg	Thr	
	210						215					220					
	CAC	CCA	TCA	GCC	ACA	CTC	CAC	AAC	CCT	ACC	CGC	GTG	AAA	CTC	TTT	GAA	720
5	His	Pro	Ser	Ala	Thr	Leu	His	Asn	Pro	Thr	Arg	Val	Lys	Leu	Phe	Glu	
	225					230				235					240		
	AAG	TGG	GGC	TGG	AAG	AAG	ATT	GCT	ACC	ATC	CAG	CAG	ACC	ACT	GAG	GTC	768
	Lys	Trp	Gly	Trp	Lys	Lys	Ile	Ala	Thr	Ile	Gln	Gln	Thr	Thr	Glu	Val	
10					245					250					255		
	TTC	ACT	TCG	ACT	CTG	GAC	GAC	CTG	GAG	GAA	CGA	GTG	AAG	GAG	GCT	GGA	816
	Phe	Thr	Ser	Thr	Leu	Asp	Asp	Leu	Glu	Glu	Arg	Val	Lys	Glu	Ala	Gly	
					260				265					270			
15																	
	ATT	GAG	ATT	ACT	TTC	CGC	CAG	AGT	TTC	TTC	TCA	GAT	CCA	GCT	GTG	CCC	864
	Ile	Glu	Ile	Thr	Phe	Arg	Gln	Ser	Phe	Phe	Ser	Asp	Pro	Ala	Val	Pro	
		275					280						285				
20																	
	GTC	AAA	AAC	CTG	AAG	CGC	CAG	GAT	GCC	CGA	ATC	ATC	GTG	GGA	CTT	TTC	912
	Val	Lys	Asn	Leu	Lys	Arg	Gln	Asp	Ala	Arg	Ile	Ile	Val	Gly	Leu	Phe	
		290					295				300						
	TAT	GAG	ACT	GAA	GCC	CGG	AAA	GTT	TTT	TGT	GAG	GTG	TAC	AAG	GAG	CGT	960
25	Tyr	Glu	Thr	Glu	Ala	Arg	Lys	Val	Phe	Cys	Glu	Val	Tyr	Lys	Glu	Arg	
	305					310					315				320		
	CTC	TTT	GGG	AAG	AAG	TAC	GTC	TGG	TTC	CTC	ATT	GGG	TGG	TAT	GCT	GAC	1008
	Leu	Phe	Gly	Lys	Lys	Tyr	Val	Trp	Phe	Leu	Ile	Gly	Trp	Tyr	Ala	Asp	
30					325					330					335		
	AAT	TGG	TTC	AAG	ATC	TAC	GAC	CCT	TCT	ATC	AAC	TGC	ACA	GTG	GAT	GAG	1056
	Asn	Trp	Phe	Lys	Ile	Tyr	Asp	Pro	Ser	Ile	Asn	Cys	Thr	Val	Asp	Glu	
				340					345					350			
35																	
	ATG	ACT	GAG	GCG	GTG	GAG	GGC	CAC	ATC	ACA	ACT	GAG	ATT	GTC	ATG	CTG	1104
	Met	Thr	Glu	Ala	Val	Glu	Gly	His	Ile	Thr	Thr	Glu	Ile	Val	Met	Leu	
		355					360					365					
40																	
	AAT	CCT	GCC	AAT	ACC	CGC	AGC	ATT	TCC	AAC	ATG	ACA	TCC	CAG	GAA	TTT	1152
	Asn	Pro	Ala	Asn	Thr	Arg	Ser	Ile	Ser	Asn	Met	Thr	Ser	Gln	Glu	Phe	
		370					375				380						

	GTG GAG AAA CTA ACC AAG CGA CTG AAA AGA CAC CCT GAG GAG ACA GGA	1200
	Val Glu Lys Leu Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr Gly	
	385 390 395 400	
5	GGC TTC CAG GAG GCA CCG CTG GCC TAT GAT GCC ATC TGG GCC TTG GCA	1248
	Gly Phe Gln Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu Ala	
	405 410 415	
	CTG GCC CTG AAC AAG ACA TCT GGA GGA GGC GGC CGT TCT GGT GTG CGC	1296
10	Leu Ala Leu Asn Lys Thr Ser Gly Gly Gly Arg Ser Gly Val Arg	
	420 425 430	
	CTG GAG GAC TTC AAC TAC AAC AAC CAG ACC ATT ACC GAC CAA ATC TAC	1344
	Leu Glu Asp Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile Tyr	
15	435 440 445	
	CGG GCA ATG AAC TCT TCG TCC TTT GAG GGT GTC TCT GGC CAT GTG GTG	1392
	Arg Ala Met Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val Val	
	450 455 460	
20	TTT GAT GCC AGC GGC TCT CGG ATG GCA TGG ACG CTT ATC GAG CAG CTT	1440
	Phe Asp Ala Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln Leu	
	465 470 475 480	
25	CAG GGT GGC AGC TAC AAG AAG ATT GGC TAC TAT GAC AGC ACC AAG GAT	1488
	Gln Gly Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys Asp	
	485 490 495	
	GAT CTT TCC TGG TCC AAA ACA GAT AAA TGG ATT GGA GGG TCC CCC CCA	1536
30	Asp Leu Ser Trp Ser Lys Thr Asp Lys Trp Ile Gly Gly Ser Pro Pro	
	500 505 510	
	GCT GAC CAG ACC CTG GTC ATC AAG ACA TTC CGC TTC CTG TCA CAG AAA	1584
	Ala Asp Gln Thr Leu Val Ile Lys Thr Phe Arg Phe Leu Ser Gln Lys	
35	515 520 525	
	CTC TTT ATC TCC GTC TCA GTT CTC TCC AGC CTG GGC ATT GTC CTA GCT	1632
	Leu Phe Ile Ser Val Ser Val Leu Ser Ser Leu Gly Ile Val Leu Ala	
	530 535 540	
40	GTT GTC TGT CTG TCC TTT AAC ATC TAC AAC TCA CAT GTC CGT TAT ATC	1680
	Val Val Cys Leu Ser Phe Asn Ile Tyr Asn Ser His Val Arg Tyr Ile	
	545 550 555 560	

	CAG AAC TCA CAG CCC AAC CTG AAC AAC CTG ACT GCT GTG GGC TGC TCA	1728
	Gln Asn Ser Gln Pro Asn Leu Asn Asn Leu Thr Ala Val Gly Cys Ser	
	565 570 575	
5	CTG GCT TTA GCT GCT GTC TTC CCC CTG GGG CTC GAT GGT TAC CAC ATT	1776
	Leu Ala Leu Ala Ala Val Phe Pro Leu Gly Leu Asp Gly Tyr His Ile	
	580 585 590	
10	GGG AGG AAC CAG TTT CCT TTC GTC TGC CAG GCC CGC CTC TGG CTC CTG	1824
	Gly Arg Asn Gln Phe Pro Phe Val Cys Gln Ala Arg Leu Trp Leu Leu	
	595 600 605	
	GGC CTG GGC TTT AGT CTG GGC TAC GGT TCC ATG TTC ACC AAG ATT TGG	1872
15	Gly Leu Gly Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr Lys Ile Trp	
	610 615 620	
	TGG GTC CAC ACG GTC TTC ACA AAG AAG GAA GAA AAG AAG GAG TGG AGG	1920
	Trp Val His Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp Arg	
20	625 630 635 640	
	AAG ACT CTG GAA CCC TGG AAG CTG TAT GCC ACA GTG GGC CTG CTG GTG	1968
	Lys Thr Leu Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly Leu Leu Val	
	645 650 655	
25	GGC ATG GAT GTC CTC ACT CTC GCC ATC TGG CAG ATC GTG GAC CCT CTG	2016
	Gly Met Asp Val Leu Thr Leu Ala Ile Trp Gln Ile Val Asp Pro Leu	
	660 665 670	
30	CAC CGG ACC ATT GAG ACA TTT GCC AAG GAG GAA CCT AAG GAA GAT ATT	2064
	His Arg Thr Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys Glu Asp Ile	
	675 680 685	
	GAC GTC TCT ATT CTG CCC CAG CTG GAG CAT TGC AGC TCC AGG AAG ATG	2112
35	Asp Val Ser Ile Leu Pro Gln Leu Glu His Cys Ser Ser Arg Lys Met	
	690 695 700	
	AAT ACA TGG CTT GGC ATT TTC TAT GGT TAC AAG GGG CTG CTG CTG CTG	2160
	Asn Thr Trp Leu Gly Ile Phe Tyr Gly Tyr Lys Gly Leu Leu Leu Leu	
40	705 710 715 720	
	CTG GGA ATC TTC CTT GCT TAT GAG ACC AAG AGT GTG TCC ACT GAG AAG	2208
	Leu Gly Ile Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser Thr Glu Lys	

	725	730	735	
	ATC AAT GAT CAC CGG GCT GTG GGC ATG GCT ATC TAC AAT GTG GCA GTC	2256		
	Ile Asn Asp His Arg Ala Val Gly Met Ala Ile Tyr Asn Val Ala Val			
5	740	745	750	
	CTG TGC CTC ATC ACT GCT CCT GTC ACC ATG ATT CTG TCC AGC CAG CAG	2304		
	Leu Cys Leu Ile Thr Ala Pro Val Thr Met Ile Leu Ser Ser Gln Gln			
	755	760	765	
10	GAT GCA GCC TTT GCC TTT GCC TCT CTT GCC ATA GTT TTC TCC TCC TAT	2352		
	Asp Ala Ala Phe Ala Phe Ala Ser Leu Ala Ile Val Phe Ser Ser Tyr			
	770	775	780	
15	ATC ACT CTT GTT GTG CTC TTT GTG CCC AAG ATG CGC AGG CTG ATC ACC	2400		
	Ile Thr Leu Val Val Leu Phe Val Pro Lys Met Arg Arg Leu Ile Thr			
	785	790	795	800
	CGA GGG GAA TGG CAG TCG GAG GCG CAG GAC ACC ATG AAG ACA GGG TCA	2448		
20	Arg Gly Glu Trp Gln Ser Glu Ala Gln Asp Thr Met Lys Thr Gly Ser			
	805	810	815	
	TCG ACC AAC AAC AAC GAG GAG GAG AAG TCC CGG CTG TTG GAG AAG GAG	2496		
	Ser Thr Asn Asn Asn Glu Glu Glu Lys Ser Arg Leu Leu Glu Lys Glu			
25	820	825	830	
	AAC CGT GAA CTG GAA AAG ATC ATT GCT GAG AAA GAG GAG CGT GTC TCT	2544		
	Asn Arg Glu Leu Glu Lys Ile Ile Ala Glu Lys Glu Glu Arg Val Ser			
	835	840	845	
30	GAA CTG CGC CAT CAA CTC CAG TCT CGG CAG CAG CTC CGC TCC CGG CGC	2592		
	Glu Leu Arg His Gln Leu Gln Ser Arg Gln Gln Leu Arg Ser Arg Arg			
	850	855	860	
35	CAC CCA CCG ACA CCC CCA GAA CCC TCT GGG GGC CTG CCC AGG GGA CCC	2640		
	His Pro Pro Thr Pro Pro Glu Pro Ser Gly Gly Leu Pro Arg Gly Pro			
	865	870	875	880
	CCT GAG CCC CCC GAC CGG CTT AGC TGT GAT GGG AGT CGA GTG CAT TTG	2688		
40	Pro Glu Pro Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg Val His Leu			
	885	890	895	
	CTT TAT AAG TGA	2700		



Leu Tyr Lys \*

## 5 (2) INFORMATION FOR SEQ ID NO: 71:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 899 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

15

Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly  
 1 5 10 15

Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile  
 20 20 25 30

Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg  
 35 40 45

25 Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu  
 50 55 60

Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys  
 65 70 75 80

30

Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys  
 85 90 95

Val Asn Arg Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly Ala  
 35 100 105 110

Leu Phe Pro Met Ser Gly Gly Trp Pro Gly Gly Gln Ala Cys Gln Pro  
 115 120 125

40 Ala Val Glu Met Ala Leu Glu Asp Val Asn Ser Arg Arg Asp Ile Leu  
 130 135 140

Pro Asp Tyr Glu Leu Lys Leu Ile His His Asp Ser Lys Cys Asp Pro

	145	150	155	160
	Gly Gln Ala Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro Ile			
	165	170	175	
5	Lys Ile Ile Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val Ala			
	180	185	190	
	Glu Ala Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser Ser			
10	195	200	205	
	Ser Pro Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg Thr			
	210	215	220	
15	His Pro Ser Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe Glu			
	225	230	235	240
	Lys Trp Gly Trp Lys Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu Val			
	245	250	255	
20	Phe Thr Ser Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala Gly			
	260	265	270	
	Ile Glu Ile Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val Pro			
25	275	280	285	
	Val Lys Asn Leu Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu Phe			
	290	295	300	
30	Tyr Glu Thr Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu Arg			
	305	310	315	320
	Leu Phe Gly Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala Asp			
	325	330	335	
35	Asn Trp Phe Lys Ile Tyr Asp Pro Ser Ile Asn Cys Thr Val Asp Glu			
	340	345	350	
	Met Thr Glu Ala Val Glu Gly His Ile Thr Thr Glu Ile Val Met Leu			
40	355	360	365	
	Asn Pro Ala Asn Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu Phe			
	370	375	380	

Val Glu Lys Leu Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr Gly  
 385 390 395 400

5 Gly Phe Gln Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu Ala  
 405 410 415

Leu Ala Leu Asn Lys Thr Ser Gly Gly Gly Gly Arg Ser Gly Val Arg  
 420 425 430

10 Leu Glu Asp Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile Tyr  
 435 440 445

Arg Ala Met Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val Val  
 15 450 455 460

Phe Asp Ala Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln Leu  
 465 470 475 480

20 Gln Gly Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys Asp  
 485 490 495

Asp Leu Ser Trp Ser Lys Thr Asp Lys Trp Ile Gly Gly Ser Pro Pro  
 500 505 510

25 Ala Asp Gln Thr Leu Val Ile Lys Thr Phe Arg Phe Leu Ser Gln Lys  
 515 520 525

Leu Phe Ile Ser Val Ser Val Leu Ser Ser Leu Gly Ile Val Leu Ala  
 30 530 535 540

Val Val Cys Leu Ser Phe Asn Ile Tyr Asn Ser His Val Arg Tyr Ile  
 545 550 555 560

35 Gln Asn Ser Gln Pro Asn Leu Asn Asn Leu Thr Ala Val Gly Cys Ser  
 565 570 575

Leu Ala Leu Ala Ala Val Phe Pro Leu Gly Leu Asp Gly Tyr His Ile  
 580 585 590

40 Gly Arg Asn Gln Phe Pro Phe Val Cys Gln Ala Arg Leu Trp Leu Leu  
 595 600 605

Gly Leu Gly Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr Lys Ile Trp  
 610 615 620

Trp Val His Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp Arg  
 5 625 630 635 640

Lys Thr Leu Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly Leu Leu Val  
 645 650 655

10 Gly Met Asp Val Leu Thr Leu Ala Ile Trp Gln Ile Val Asp Pro Leu  
 660 665 670

His Arg Thr Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys Glu Asp Ile  
 675 680 685

15 Asp Val Ser Ile Leu Pro Gln Leu Glu His Cys Ser Ser Arg Lys Met  
 690 695 700

Asn Thr Trp Leu Gly Ile Phe Tyr Gly Tyr Lys Gly Leu Leu Leu Leu  
 20 705 710 715 720

Leu Gly Ile Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser Thr Glu Lys  
 725 730 735

25 Ile Asn Asp His Arg Ala Val Gly Met Ala Ile Tyr Asn Val Ala Val  
 740 745 750

Leu Cys Leu Ile Thr Ala Pro Val Thr Met Ile Leu Ser Ser Gln Gln  
 755 760 765

30 Asp Ala Ala Phe Ala Phe Ala Ser Leu Ala Ile Val Phe Ser Ser Tyr  
 770 775 780

Ile Thr Leu Val Val Leu Phe Val Pro Lys Met Arg Arg Leu Ile Thr  
 35 785 790 795 800

Arg Gly Glu Trp Gln Ser Glu Ala Gln Asp Thr Met Lys Thr Gly Ser  
 805 810 815

40 Ser Thr Asn Asn Asn Glu Glu Glu Lys Ser Arg Leu Leu Glu Lys Glu  
 820 825 830

Asn Arg Glu Leu Glu Lys Ile Ile Ala Glu Lys Glu Glu Arg Val Ser

835 840 845

Glu Leu Arg His Gln Leu Gln Ser Arg Gln Gln Leu Arg Ser Arg Arg  
 850 855 860

5 His Pro Pro Thr Pro Pro Glu Pro Ser Gly Gly Leu Pro Arg Gly Pro  
 865 870 875 880

Pro Glu Pro Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg Val His Leu  
 10 885 890 895

Leu Tyr Lys

15

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2518 base pairs  
 20 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

25

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens  
 30

(ix) FEATURE:

(A) NAME/KEY: CDS  
 (B) LOCATION:1..294

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

ATG TTG CTG CTG CTG CTA CTG GCG CCA CTC TTC CTC CGC CCC CCG GGC 48  
 Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly  
 40 1 5 10 15

GCG GGC GGG GCG CAG ACC CCC AAC GCC ACC TCA GAA GGT TGC CAG ATC 96  
 Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile

	20	25	30	
	ATA CAC CCG CCC TGG GAA GGG GGC ATC AGG TAC CGG GGC CTG ACT CGG			144
	Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg			
5	35	40	45	
	GAC CAG GTG AAG GCT ATC AAC TTC CTG CCA GTG GAC TAT GAG ATT GAG			192
	Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu			
	50	55	60	
10	TAT GTG TGC CGG GGG GAG CGC GAG GTG GTG GGG CCC AAG GTC CGC AAG			240
	Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys			
	65	70	75	80
15	TGC CTG GCC AAC GGC TCC TGG ACA GAT ATG GAC ACA CCC AGC CGC TGT			288
	Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys			
	85	90	95	
	GTG TGA TCCAGGCCAA GCCACCAAGT ACCTATATGA GCTGCTCTAC AACGACCCTA			344
20	Val *			
	TCAAGATCAT CCTTATGCCT GGCTGCAGCT CTGTCTCCAC GCTGGTGGCT GAGGCTGCTA			404
25	GGATGTGGAA CCTCATTTGTG CTTTCCTATG GCTCCAGCTC ACCAGCCCTG TCAAACCGGC			464
	AGCGTTTCCC CACTTTCTTC CGAACGCACC CATCAGCCAC ACTCCACAAC CCTACCCGCG			524
	TGAAACTCTT TGAAAAGTGG GGCTGGAAGA AGATTGCTAC CATCCAGCAG ACCACTGAGG			584
30	TCTTCACTTC GACTCTGGAC GACCTGGAGG AACGAGTGAA GGAGGCTGGA ATTGAGATTA			644
	CTTTCCGCCA GAGTTTCTTC TCAGATCCAG CTGTGCCCCGT CAAAACCTG AAGCGCCAGG			704
35	ATGCCCCAAT CATCGTGGGA CTTTCTATG AGACTGAAGC CCGGAAAGTT TTTTGTGAGG			764
	TGTACAAGGA GCGTCTCTTT GGGAAGAAGT ACGTCTGGTT CCTCATTTGGG TGGTATGCTG			824
	ACAATTGGTT CAAGATCTAC GACCCTTCTA TCAACTGCAC AGTGGATGAG ATGACTGAGG			884
40	CGGTGGAGGG CCACATCACA ACTGAGATTG TCATGCTGAA TCCTGCCAAT ACCCGCAGCA			944
	TTTCCAACAT GACATCCCAG GAATTTGTGG AGAACTAAC CAAGCGACTG AAAAGACACC			1004

	CTGAGGAGAC	AGGAGGCTTC	CAGGAGGCAC	CGCTGGCCTA	TGATGCCATC	TGGGCCTTGG	1064
	CACTGGCCCT	GAACAAGACA	TCTGGAGGAG	GCGGCCGTTC	TGGTGTGCGC	CTGGAGGACT	1124
5	TCAACTACAA	CAACCAGACC	ATTACCGACC	AAATCTACCG	GGCAATGAAC	TCTTCGTCCT	1184
	TTGAGGGTGT	CTCTGGCCAT	GTGGTGTTTG	ATGCCAGCGG	CTCTCGGATG	GCATGGACGC	1244
10	TTATCGAGCA	GCTTCAGGGT	GGCAGCTACA	AGAAGATTGG	CTACTATGAC	AGCACCAAGG	1304
	ATGATCTTTC	CTGGTCCAAA	ACAGATAAAT	GGATTGGAGG	GTCCCCCCCCA	GCTGACCAGA	1364
	CCCTGGTCAT	CAAGACATTC	CGCTTCCTGT	CACAGAAACT	CTTTATCTCC	GTCTCAGTTC	1424
15	TCTCCAGCCT	GGGCATTGTC	CTAGCTGTTG	TCTGTCTGTC	CTTTAACATC	TACAACTCAC	1484
	ATGTCCGTTA	TATCCAGAAC	TCACAGCCCA	ACCTGAACAA	CCTGACTGCT	GTGGGCTGCT	1544
20	CACTGGCTTT	AGCTGCTGTC	TTCCCCCTGG	GGCTCGATGG	TTACCACATT	GGGAGGAACC	1604
	AGTTTCCTTT	CGTCTGCCAG	GCCCGCCTCT	GGCTCCTGGG	CCTGGGCTTT	AGTCTGGGCT	1664
	ACGGTTCCAT	GTTACCAAG	ATTTGGTGGG	TCCACACGGT	CTTCACAAAG	AAGGAAGAAA	1724
25	AGAAGGAGTG	GAGGAAGACT	CTGGAACCCT	GGAAGCTGTA	TGCCACAGTG	GGCCTGCTGG	1784
	TGGGCATGGA	TGTCCTCACT	CTCGCCATCT	GGCAGATCGT	GGACCCCTCTG	CACCGGACCA	1844
30	TTGAGACATT	TGCCAAGGAG	GAACCTAAGG	AAGATATTGA	CGTCTCTATT	CTGCCCCAGC	1904
	TGGAGCATTG	CAGCTCCAGG	AAGATGAATA	CATGGCTTGG	CATTTTCTAT	GGTTACAAGG	1964
	GGCTGCTGCT	GCTGCTGGGA	ATCTTCCTTG	CTTATGAGAC	CAAGAGTGTG	TCCACTGAGA	2024
35	AGATCAATGA	TCACCGGGCT	GTGGGCATGG	CTATCTACAA	TGTGGCAGTC	CTGTGCCTCA	2084
	TCACTGCTCC	TGTCACCATG	ATTCTGTCCA	GCCAGCAGGA	TGCAGCCTTT	GCCTTTGCCT	2144
40	CTCTTGCCAT	AGTTTTCTCC	TCCTATATCA	CTCTTGTTGT	GCTCTTTGTG	CCCAAGATGC	2204
	GCAGGCTGAT	CACCCGAGGG	GAATGGCAGT	CGGAGGCGCA	GGACACCATG	AAGACAGGGT	2264

CATCGACCAA CAACAACGAG GAGGAGAAGT CCCGGCTGTT GGAGAAGGAG AACCGTGAAC 2374  
 TGGAAAAGAT CATTGCTGAG AAAGAGGAGC GTGTCTCTGA ACTGCGCCAT CAACTCCAGT 2384  
 5 CTCGGCAGCA GCTCCGCTCC CGGCGCCACC CACCGACACC CCCAGAACCC TCTGGGGGCC 2444  
 TGCCCAGGGG ACCCCCTGAG CCCCCGACC GGCTTAGCTG TGATGGGAGT CGAGTGCATT 2504  
 TGCTTTATAA GTGA 2518

10

## (2) INFORMATION FOR SEQ ID NO: 73:

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 97 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

Met Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly  
 1 5 10 15  
 25 Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile  
 20 25 30  
 Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg  
 30 35 40 45  
 Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu  
 50 55 60  
 35 Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys  
 65 70 75 80  
 Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys  
 85 90 95  
 40 Val



## (2) INFORMATION FOR SEQ ID NO: 74:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 2679 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## 10 (ii) MOLECULE TYPE: cDNA to mRNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

15

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (ix) FEATURE:

20

(A) NAME/KEY: CDS

(B) LOCATION:1..2679

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

25	ATG TTG CTG CTG CTG CTA CTG GCG CCA CTC TTC CTC CGC CCC CCG GGC	48
	Met Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly	
	1 5 10 15	
	GCG GGC GGG GCG CAG ACC CCC AAC GCC ACC TCA GAA GGT TGC CAG ATC	96
30	Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile	
	20 25 30	
	ATA CAC CCG CCC TGG GAA GGG GGC ATC AGG TAC CGG GGC CTG ACT CGG	144
	Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg	
35	35 40 45	
	GAC CAG GTG AAG GCT ATC AAC TTC CTG CCA GTG GAC TAT GAG ATT GAG	192
	Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu	
	50 55 60	
40	TAT GTG TGC CGG GGG GAG CGC GAG GTG GTG GGG CCC AAG GTC CGC AAG	240
	Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys	
	65 70 75 80	

	TGC CTG GCC AAC GGC TCC TGG ACA GAT ATG GAC ACA CCC AGC CGC TGT	288
	Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys	
	85 90 95	
5	GAA CGG CGC GCA GTG TAC ATC GGG GCA CTG TTT CCC ATG AGC GGG GGC	336
	Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe Pro Met Ser Gly Gly	
	100 105 110	
10	TGG CCA GGG GGC CAG GCC TGC CAG CCC GCG GTG GAG ATG GCG CTG GAG	384
	Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val Glu Met Ala Leu Glu	
	115 120 125	
	GAC GTG AAT AGC CGC AGG GAC ATC CTG CCG GAC TAT GAG CTC AAG CTC	432
15	Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp Tyr Glu Leu Lys Leu	
	130 135 140	
	ATC CAC CAC GAC AGC AAG TGT GAT CCA GGC CAA GCC ACC AAG TAC CTA	480
	Ile His His Asp Ser Lys Cys Asp Pro Gly Gln Ala Thr Lys Tyr Leu	
20	145 150 155 160	
	TAT GAG CTG CTC TAC AAC GAC CCT ATC AAG ATC ATC CTT ATG CCT GGC	528
	Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile Ile Leu Met Pro Gly	
	165 170 175	
25	TGC AGC TCT GTC TCC ACG CTG GTG GCT GAG GCT GCT AGG ATG TGG AAC	576
	Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala Arg Met Trp Asn	
	180 185 190	
30	CTC ATT GTG CTT TCC TAT GGC TCC AGC TCA CCA GCC CTG TCA AAC CGG	624
	Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala Leu Ser Asn Arg	
	195 200 205	
	CAG CGT TTC CCC ACT TTC TTC CGA ACG CAC CCA TCA GCC ACA CTC CAC	672
35	Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro Ser Ala Thr Leu His	
	210 215 220	
	AAC CCT ACC CGC GTG AAA CTC TTT GAA AAG TGG GGC TGG AAG AAG ATT	720
	Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp Gly Trp Lys Lys Ile	
40	225 230 235 240	
	GCT ACC ATC CAG CAG ACC ACT GAG GTC TTC ACT TCG ACT CTG GAC GAC	768
	Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr Ser Thr Leu Asp Asp	

	245	250	255	
	CTG GAG GAA CGA GTG AAG GAG GCT GGA ATT GAG ATT ACT TTC CGC CAG			816
	Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu Ile Thr Phe Arg Gln			
5	260	265	270	
	AGT TTC TTC TCA GAT CCA GCT GTG CCC GTC AAA AAC CTG AAG CGC CAG			864
	Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys Asn Leu Lys Arg Gln			
	275	280	285	
10	GAT GCC CGA ATC ATC GTG GGA CTT TTC TAT GAG ACT GAA GCC CGG AAA			912
	Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu Thr Glu Ala Arg Lys			
	290	295	300	
15	GTT TTT TGT GAG GTG TAC AAG GAG CGT CTC TTT GGG AAG AAG TAC GTC			960
	Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly Lys Lys Tyr Val			
	305	310	315	320
	TGG TTC CTC ATT GGG TGG TAT GCT GAC AAT TGG TTC AAG ATC TAC GAC			1008
20	Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe Lys Ile Tyr Asp			
	325	330	335	
	CCT TCT ATC AAC TGC ACA GTG GAT GAG ATG ACT GAG GCG GTG GAG GGC			1056
	Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr Glu Ala Val Glu Gly			
25	340	345	350	
	CAC ATC ACA ACT GAG ATT GTC ATG CTG AAT CCT GCC AAT ACC CGC AGC			1104
	His Ile Thr Thr Glu Ile Val Met Leu Asn Pro Ala Asn Thr Arg Ser			
	355	360	365	
30	ATT TCC AAC ATG ACA TCC CAG GAA TTT GTG GAG AAA CTA ACC AAG CGA			1152
	Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu Lys Leu Thr Lys Arg			
	370	375	380	
35	CTG AAA AGA CAC CCT GAG GAG ACA GGA GGC TTC CAG GAG GCA CCG CTG			1200
	Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln Glu Ala Pro Leu			
	385	390	395	400
	GCC TAT GAT GCC ATC TGG GCC TTG GCA CTG GCC CTG AAC AAG ACA TCT			1248
40	Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Leu Asn Lys Thr Ser			
	405	410	415	
	GGA GGA GGC GGC CGT TCT GGT GTG CGC CTG GAG GAC TTC AAC TAC AAC			1296

	Gly	Gly	Gly	Gly	Arg	Ser	Gly	Val	Arg	Leu	Glu	Asp	Phe	Asn	Tyr	Asn	
				420					425					430			
	AAC	CAG	ACC	ATT	ACC	GAC	CAA	ATC	TAC	CGG	GCA	ATG	AAC	TCT	TCG	TCC	1344
5	Asn	Gln	Thr	Ile	Thr	Asp	Gln	Ile	Tyr	Arg	Ala	Met	Asn	Ser	Ser	Ser	
			435					440					445				
	TTT	GAG	GGT	GTC	TCT	GGC	CAT	GTG	GTG	TTT	GAT	GCC	AGC	GGC	TCT	CGG	1392
	Phe	Glu	Gly	Val	Ser	Gly	His	Val	Val	Phe	Asp	Ala	Ser	Gly	Ser	Arg	
10		450					455				460						
	ATG	GCA	TGG	ACG	CTT	ATC	GAG	CAG	CTT	CAG	GGT	GGC	AGC	TAC	AAG	AAG	1440
	Met	Ala	Trp	Thr	Leu	Ile	Glu	Gln	Leu	Gln	Gly	Gly	Ser	Tyr	Lys	Lys	
	465					470				475						480	
15																	
	ATT	GGC	TAC	TAT	GAC	AGC	ACC	AAG	GAT	GAT	CTT	TCC	TGG	TCC	AAA	ACA	1488
	Ile	Gly	Tyr	Tyr	Asp	Ser	Thr	Lys	Asp	Asp	Leu	Ser	Trp	Ser	Lys	Thr	
					485					490					495		
	GAT	AAA	TGG	ATT	GGA	GGG	TCC	CCC	CCA	GCT	GAC	CAG	ACC	CTG	GTC	ATC	1536
20	Asp	Lys	Trp	Ile	Gly	Gly	Ser	Pro	Pro	Ala	Asp	Gln	Thr	Leu	Val	Ile	
				500					505					510			
	AAG	ACA	TTC	CGC	TTC	CTG	TCA	CAG	AAA	CTC	TTT	ATC	TCC	GTC	TCA	GTT	1584
25	Lys	Thr	Phe	Arg	Phe	Leu	Ser	Gln	Lys	Leu	Phe	Ile	Ser	Val	Ser	Val	
			515					520					525				
	CTC	TCC	AGC	CTG	GGC	ATT	GTC	CTA	GCT	GTT	GTC	TGT	CTG	TCC	TTT	AAC	1632
	Leu	Ser	Ser	Leu	Gly	Ile	Val	Leu	Ala	Val	Val	Cys	Leu	Ser	Phe	Asn	
30		530					535					540					
	ATC	TAC	AAC	TCA	CAT	GTC	CGT	TAT	ATC	CAG	AAC	TCA	CAG	CCC	AAC	CTG	1680
	Ile	Tyr	Asn	Ser	His	Val	Arg	Tyr	Ile	Gln	Asn	Ser	Gln	Pro	Asn	Leu	
	545					550				555					560		
35																	
	AAC	AAC	CTG	ACT	GCT	GTG	GGC	TGC	TCA	CTG	GCT	TTA	GCT	GCT	GTC	TTC	1728
	Asn	Asn	Leu	Thr	Ala	Val	Gly	Cys	Ser	Leu	Ala	Leu	Ala	Ala	Val	Phe	
					565					570					575		
	CCC	CTG	GGG	CTC	GAT	GGT	TAC	CAC	ATT	GGG	AGG	AAC	CAG	TTT	CCT	TTC	1776
40	Pro	Leu	Gly	Leu	Asp	Gly	Tyr	His	Ile	Gly	Arg	Asn	Gln	Phe	Pro	Phe	
				580					585					590			

	GTC TGC CAG GCC CGC CTC TGG CTC CTG GGC CTG GGC TTT AGT CTG GGC	1874
	Val Cys Gln Ala Arg Leu Trp Leu Leu Gly Leu Gly Phe Ser Leu Gly	
	595 600 605	
5	TAC GGT TCC ATG TTC ACC AAG ATT TGG TGG GTC CAC ACG GTC TTC ACA	1872
	Tyr Gly Ser Met Phe Thr Lys Ile Trp Trp Val His Thr Val Phe Thr	
	610 615 620	
	AAG AAG GAA GAA AAG AAG GAG TGG AGG AAG ACT CTG GAA CCC TGG AAG	1920
10	Lys Lys Glu Glu Lys Lys Glu Trp Arg Lys Thr Leu Glu Pro Trp Lys	
	625 630 635 640	
	CTG TAT GCC ACA GTG GGC CTG CTG GTG GGC ATG GAT GTC CTC ACT CTC	1968
	Leu Tyr Ala Thr Val Gly Leu Leu Val Gly Met Asp Val Leu Thr Leu	
15	645 650 655	
	GCC ATC TGG CAG ATC GTG GAC CCT CTG CAC CGG ACC ATT GAG ACA TTT	2016
	Ala Ile Trp Gln Ile Val Asp Pro Leu His Arg Thr Ile Glu Thr Phe	
	660 665 670	
20	GCC AAG GAG GAA CCT AAG GAA GAT ATT GAC GTC TCT ATT CTG CCC CAG	2064
	Ala Lys Glu Glu Pro Lys Glu Asp Ile Asp Val Ser Ile Leu Pro Gln	
	675 680 685	
25	CTG GAG CAT TGC AGC TCC AGG AAG ATG AAT ACA TGG CTT GGC ATT TTC	2112
	Leu Glu His Cys Ser Ser Arg Lys Met Asn Thr Trp Leu Gly Ile Phe	
	690 695 700	
	TAT GGT TAC AAG GGG CTG CTG CTG CTG CTG GGA ATC TTC CTT GCT TAT	2160
30	Tyr Gly Tyr Lys Gly Leu Leu Leu Leu Leu Gly Ile Phe Leu Ala Tyr	
	705 710 715 720	
	GAG ACC AAG AGT GTG TCC ACT GAG AAG ATC AAT GAT CAC CGG GCT GTG	2208
	Glu Thr Lys Ser Val Ser Thr Glu Lys Ile Asn Asp His Arg Ala Val	
35	725 730 735	
	GGC ATG GCT ATC TAC AAT GTG GCA GTC CTG TGC CTC ATC ACT GCT CCT	2256
	Gly Met Ala Ile Tyr Asn Val Ala Val Leu Cys Leu Ile Thr Ala Pro	
	740 745 750	
40	GTC ACC ATG ATT CTG TCC AGC CAG CAG GAT GCA GCC TTT GCC TTT GCC	2304
	Val Thr Met Ile Leu Ser Ser Gln Gln Asp Ala Ala Phe Ala Phe Ala	
	755 760 765	

TCT CTT GCC ATA GTT TTC TCC TCC TAT ATC ACT CTT GTT GTG CTC TTT 2352  
 Ser Leu Ala Ile Val Phe Ser Ser Tyr Ile Thr Leu Val Val Leu Phe  
 770 775 780

5

GTG CCC AAG ATG CGC AGG CTG ATC ACC CGA GGG GAA TGG CAG TCG GAG 2400  
 Val Pro Lys Met Arg Arg Leu Ile Thr Arg Gly Glu Trp Gln Ser Glu  
 785 790 795 800

10

GCG CAG GAC ACC ATG AAG ACA GGG TCA TCG ACC AAC AAC AAC GAG GAG 2448  
 Ala Gln Asp Thr Met Lys Thr Gly Ser Ser Thr Asn Asn Asn Glu Glu  
 805 810 815

15

GAG AAG TCC CGG CTG TTG GAG AAG GAG AAC CGT GAA CTG GAA AAG ATC 2496  
 Glu Lys Ser Arg Leu Leu Glu Lys Glu Asn Arg Glu Leu Glu Lys Ile  
 820 825 830

20

ATT GCT GAG AAA GAG GAG CGT GTC TCT GAA CTG CGC CAT CAA CTC CAG 2544  
 Ile Ala Glu Lys Glu Glu Arg Val Ser Glu Leu Arg His Gln Leu Gln  
 835 840 845

25

TCT CGG CAG CAG CTC CGC TCC CGG CGC CAC CCA CCG ACA CCC CCA GAA 2592  
 Ser Arg Gln Gln Leu Arg Ser Arg Arg His Pro Pro Thr Pro Pro Glu  
 850 855 860

30

AGC TGT GAT GGG AGT CGA GTG CAT TTG CTT TAT AAG TGA 2679  
 Ser Cys Asp Gly Ser Arg Val His Leu Leu Tyr Lys \*  
 885 890

35 (2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 892 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly  
 1 5 10 15  
 5  
 Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile  
 20 25 30  
 Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg  
 10 35 40 45  
 Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu  
 50 55 60  
 15 Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys  
 65 70 75 80  
 Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys  
 85 90 95  
 20  
 Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe Pro Met Ser Gly Gly  
 100 105 110  
 Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val Glu Met Ala Leu Glu  
 25 115 120 125  
 Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp Tyr Glu Leu Lys Leu  
 130 135 140  
 30 Ile His His Asp Ser Lys Cys Asp Pro Gly Gln Ala Thr Lys Tyr Leu  
 145 150 155 160  
 Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile Ile Leu Met Pro Gly  
 165 170 175  
 35  
 Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala Arg Met Trp Asn  
 180 185 190  
 Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala Leu Ser Asn Arg  
 40 195 200 205  
 Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro Ser Ala Thr Leu His  
 210 215 220

Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp Gly Trp Lys Lys Ile  
 225 230 235 240

5 Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr Ser Thr Leu Asp Asp  
 245 250 255

Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu Ile Thr Phe Arg Gln  
 260 265 270

10 Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys Asn Leu Lys Arg Gln  
 275 280 285

Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu Thr Glu Ala Arg Lys  
 15 290 295 300

Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly Lys Lys Tyr Val  
 305 310 315 320

20 Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe Lys Ile Tyr Asp  
 325 330 335

Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr Glu Ala Val Glu Gly  
 340 345 350

25 His Ile Thr Thr Glu Ile Val Met Leu Asn Pro Ala Asn Thr Arg Ser  
 355 360 365

Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu Lys Leu Thr Lys Arg  
 30 370 375 380

Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln Glu Ala Pro Leu  
 385 390 395 400

35 Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Leu Asn Lys Thr Ser  
 405 410 415

Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu Asp Phe Asn Tyr Asn  
 420 425 430

40 Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala Met Asn Ser Ser Ser  
 435 440 445



Phe Glu Gly Val Ser Gly His Val Val Phe Asp Ala Ser Gly Ser Arg  
 450 455 460

Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly Gly Ser Tyr Lys Lys  
 5 465 470 475 480

Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu Ser Trp Ser Lys Thr  
 485 490 495

10 Asp Lys Trp Ile Gly Gly Ser Pro Pro Ala Asp Gln Thr Leu Val Ile  
 500 505 510

Lys Thr Phe Arg Phe Leu Ser Gln Lys Leu Phe Ile Ser Val Ser Val  
 515 520 525

15 Leu Ser Ser Leu Gly Ile Val Leu Ala Val Val Cys Leu Ser Phe Asn  
 530 535 540

Ile Tyr Asn Ser His Val Arg Tyr Ile Gln Asn Ser Gln Pro Asn Leu  
 20 545 550 555 560

Asn Asn Leu Thr Ala Val Gly Cys Ser Leu Ala Leu Ala Ala Val Phe  
 565 570 575

25 Pro Leu Gly Leu Asp Gly Tyr His Ile Gly Arg Asn Gln Phe Pro Phe  
 580 585 590

Val Cys Gln Ala Arg Leu Trp Leu Leu Gly Leu Gly Phe Ser Leu Gly  
 595 600 605

30 Tyr Gly Ser Met Phe Thr Lys Ile Trp Trp Val His Thr Val Phe Thr  
 610 615 620

Lys Lys Glu Glu Lys Lys Glu Trp Arg Lys Thr Leu Glu Pro Trp Lys  
 35 625 630 635 640

Leu Tyr Ala Thr Val Gly Leu Leu Val Gly Met Asp Val Leu Thr Leu  
 645 650 655

40 Ala Ile Trp Gln Ile Val Asp Pro Leu His Arg Thr Ile Glu Thr Phe  
 660 665 670

Ala Lys Glu Glu Pro Lys Glu Asp Ile Asp Val Ser Ile Leu Pro Gln

	675	680	685
	Leu Glu His Cys Ser Ser Arg Lys Met Asn Thr Trp Leu Gly Ile Phe		
	690	695	700
5	Tyr Gly Tyr Lys Gly Leu Leu Leu Leu Gly Ile Phe Leu Ala Tyr		
	705	710	715 720
	Glu Thr Lys Ser Val Ser Thr Glu Lys Ile Asn Asp His Arg Ala Val		
10	725	730	735
	Gly Met Ala Ile Tyr Asn Val Ala Val Leu Cys Leu Ile Thr Ala Pro		
	740	745	750
15	Val Thr Met Ile Leu Ser Ser Gln Gln Asp Ala Ala Phe Ala Phe Ala		
	755	760	765
	Ser Leu Ala Ile Val Phe Ser Ser Tyr Ile Thr Leu Val Val Leu Phe		
	770	775	780
20	Val Pro Lys Met Arg Arg Leu Ile Thr Arg Gly Glu Trp Gln Ser Glu		
	785	790	795 800
	Ala Gln Asp Thr Met Lys Thr Gly Ser Ser Thr Asn Asn Asn Glu Glu		
25	805	810	815
	Glu Lys Ser Arg Leu Leu Glu Lys Glu Asn Arg Glu Leu Glu Lys Ile		
	820	825	830
30	Ile Ala Glu Lys Glu Glu Arg Val Ser Glu Leu Arg His Gln Leu Gln		
	835	840	845
	Ser Arg Gln Gln Leu Arg Ser Arg Arg His Pro Pro Thr Pro Pro Glu		
	850	855	860
35	Pro Ser Gly Gly Leu Pro Arg Gly Pro Pro Glu Pro Pro Asp Arg Leu		
	865	870	875 880
	Ser Cys Asp Gly Ser Arg Val His Leu Leu Tyr Lys		
40	885	890	

(2) INFORMATION FOR SEQ ID NO: 76:

H1865-1 WO SEQ

145

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2661 base pairs

(B) TYPE: nucleic acid

5 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA to mRNA

10 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

15 (A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..2661

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

	ATG	TTG	CTG	CTG	CTA	CTG	GCG	CCA	CTC	TTC	CTC	GCG	CCC	CCG	GGC	48	
	Met	Leu	Leu	Leu	Leu	Leu	Ala	Pro	Leu	Phe	Leu	Arg	Pro	Pro	Gly		
25	1				5				10						15		
	GCG	GGC	GGG	GCG	CAG	ACC	CCC	AAC	GCC	ACC	TCA	GAA	GGT	TGC	CAG	ATC	96
	Ala	Gly	Gly	Ala	Gln	Thr	Pro	Asn	Ala	Thr	Ser	Glu	Gly	Cys	Gln	Ile	
				20				25						30			
30	ATA	CAC	CCG	CCC	TGG	GAA	GGG	GCG	ATC	AGG	TAC	CGG	GGC	CTG	ACT	CGG	144
	Ile	His	Pro	Pro	Trp	Glu	Gly	Gly	Ile	Arg	Tyr	Arg	Gly	Leu	Thr	Arg	
			35					40					45				
35	GAC	CAG	GTG	AAG	GCT	ATC	AAC	TTC	CTG	CCA	GTG	GAC	TAT	GAG	ATT	GAG	192
	Asp	Gln	Val	Lys	Ala	Ile	Asn	Phe	Leu	Pro	Val	Asp	Tyr	Glu	Ile	Glu	
			50					55					60				
	TAT	GTG	TGC	CGG	GGG	GAG	CGC	GAG	GTG	GTG	GGG	CCC	AAG	GTC	CGC	AAG	240
40	Tyr	Val	Cys	Arg	Gly	Glu	Arg	Glu	Val	Val	Gly	Pro	Lys	Val	Arg	Lys	
	65					70					75					80	
	TGC	CTG	GCC	AAC	GGC	TCC	TGG	ACA	GAT	ATG	GAC	ACA	CCC	AGC	CGC	TGT	288

	Cys	Leu	Ala	Asn	Gly	Ser	Trp	Thr	Asp	Met	Asp	Thr	Pro	Ser	Arg	Cys	
	85								90				95				
	GTG	AAT	CGA	ACG	CCA	CAC	TCA	GAA	CGG	CGC	GCA	GTG	TAC	ATC	GGG	GCA	336
5	Val	Asn	Arg	Thr	Pro	His	Ser	Glu	Arg	Arg	Ala	Val	Tyr	Ile	Gly	Ala	
	100				105				110								
	CTG	TTT	CCC	GCG	GTG	GAG	ATG	GCG	CTG	GAG	GAC	GTG	AAT	AGC	CGC	AGG	384
10	Leu	Phe	Pro	Ala	Val	Glu	Met	Ala	Leu	Glu	Asp	Val	Asn	Ser	Arg	Arg	
	115				120				125								
	GAC	ATC	CTG	CCG	GAC	TAT	GAG	CTC	AAG	CTC	ATC	CAC	CAC	GAC	AGC	AAG	432
	Asp	Ile	Leu	Pro	Asp	Tyr	Glu	Leu	Lys	Leu	Ile	His	His	Asp	Ser	Lys	
	130				135				140								
15	TGT	GAT	CCA	GGC	CAA	GCC	ACC	AAG	TAC	CTA	TAT	GAG	CTG	CTC	TAC	AAC	480
	Cys	Asp	Pro	Gly	Gln	Ala	Thr	Lys	Tyr	Leu	Tyr	Glu	Leu	Leu	Tyr	Asn	
	145				150				155				160				
20	GAC	CCT	ATC	AAG	ATC	ATC	CTT	ATG	CCT	GGC	TGC	AGC	TCT	GTC	TCC	ACG	528
	Asp	Pro	Ile	Lys	Ile	Ile	Leu	Met	Pro	Gly	Cys	Ser	Ser	Val	Ser	Thr	
	165				170				175								
	CTG	GTG	GCT	GAG	GCT	GCT	AGG	ATG	TGG	AAC	CTC	ATT	GTG	CTT	TCC	TAT	576
25	Leu	Val	Ala	Glu	Ala	Ala	Arg	Met	Trp	Asn	Leu	Ile	Val	Leu	Ser	Tyr	
	180				185				190								
	GGC	TCC	AGC	TCA	CCA	GCC	CTG	TCA	AAC	CGG	CAG	CGT	TTC	CCC	ACT	TTC	624
30	Gly	Ser	Ser	Ser	Pro	Ala	Leu	Ser	Asn	Arg	Gln	Arg	Phe	Pro	Thr	Phe	
	195				200				205								
	TTC	CGA	ACG	CAC	CCA	TCA	GCC	ACA	CTC	CAC	AAC	CCT	ACC	CGC	GTG	AAA	672
	Phe	Arg	Thr	His	Pro	Ser	Ala	Thr	Leu	His	Asn	Pro	Thr	Arg	Val	Lys	
	210				215				220								
35	CTC	TTT	GAA	AAG	TGG	GGC	TGG	AAG	AAG	ATT	GCT	ACC	ATC	CAG	CAG	ACC	720
	Leu	Phe	Glu	Lys	Trp	Gly	Trp	Lys	Lys	Ile	Ala	Thr	Ile	Gln	Gln	Thr	
	225				230				235				240				
40	ACT	GAG	GTC	TTC	ACT	TCG	ACT	CTG	GAC	GAC	CTG	GAG	GAA	CGA	GTG	AAG	768
	Thr	Glu	Val	Phe	Thr	Ser	Thr	Leu	Asp	Asp	Leu	Glu	Glu	Arg	Val	Lys	
	245				250				255								

	GAG GCT GGA ATT GAG ATT ACT TTC CGC CAG AGT TTC TTC TCA GAT CCA	816
	Glu Ala Gly Ile Glu Ile Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro	
	260 265 270	
5	GCT GTG CCC GTC AAA AAC CTG AAG CGC CAG GAT GCC CGA ATC ATC GTG	864
	Ala Val Pro Val Lys Asn Leu Lys Arg Gln Asp Ala Arg Ile Ile Val	
	275 280 285	
10	GGA CTT TTC TAT GAG ACT GAA GCC CGG AAA GTT TTT TGT GAG GTG TAC	912
	Gly Leu Phe Tyr Glu Thr Glu Ala Arg Lys Val Phe Cys Glu Val Tyr	
	290 295 300	
15	AAG GAG CGT CTC TTT GGG AAG AAG TAC GTC TGG TTC CTC ATT GGG TGG	960
	Lys Glu Arg Leu Phe Gly Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp	
	305 310 315 320	
20	TAT GCT GAC AAT TGG TTC AAG ATC TAC GAC CCT TCT ATC AAC TGC ACA	1008
	Tyr Ala Asp Asn Trp Phe Lys Ile Tyr Asp Pro Ser Ile Asn Cys Thr	
	325 330 335	
	GTG GAT GAG ATG ACT GAG GCG GTG GAG GGC CAC ATC ACA ACT GAG ATT	1056
	Val Asp Glu Met Thr Glu Ala Val Glu Gly His Ile Thr Thr Glu Ile	
	340 345 350	
25	GTC ATG CTG AAT CCT GCC AAT ACC CGC AGC ATT TCC AAC ATG ACA TCC	1104
	Val Met Leu Asn Pro Ala Asn Thr Arg Ser Ile Ser Asn Met Thr Ser	
	355 360 365	
30	CAG GAA TTT GTG GAG AAA CTA ACC AAG CGA CTG AAA AGA CAC CCT GAG	1152
	Gln Glu Phe Val Glu Lys Leu Thr Lys Arg Leu Lys Arg His Pro Glu	
	370 375 380	
35	GAG ACA GGA GGC TTC CAG GAG GCA CCG CTG GCC TAT GAT GCC ATC TGG	1200
	Glu Thr Gly Gly Phe Gln Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp	
	385 390 395 400	
40	GCC TTG GCA CTG GCC CTG AAC AAG ACA TCT GGA GGA GGC GGC CGT TCT	1248
	Ala Leu Ala Leu Ala Leu Asn Lys Thr Ser Gly Gly Gly Gly Arg Ser	
	405 410 415	
	GGT GTG CGC CTG GAG GAC TTC AAC TAC AAC AAC CAG ACC ATT ACC GAC	1296
	Gly Val Arg Leu Glu Asp Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp	
	420 425 430	

	CAA ATC TAC CGG GCA ATG AAC TCT TCG TCC TTT GAG GGT GTC TCT GGC	1344
	Gln Ile Tyr Arg Ala Met Asn Ser Ser Ser Phe Glu Gly Val Ser Gly	
	435 440 445	
5	CAT GTG GTG TTT GAT GCC AGC GGC TCT CGG ATG GCA TGG ACG CTT ATC	1392
	His Val Val Phe Asp Ala Ser Gly Ser Arg Met Ala Trp Thr Leu Ile	
	450 455 460	
10	GAG CAG CTT CAG GGT GGC AGC TAC AAG AAG ATT GGC TAC TAT GAC AGC	1440
	Glu Gln Leu Gln Gly Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser	
	465 470 475 480	
	ACC AAG GAT GAT CTT TCC TGG TCC AAA ACA GAT AAA TGG ATT GGA GGG	1488
15	Thr Lys Asp Asp Leu Ser Trp Ser Lys Thr Asp Lys Trp Ile Gly Gly	
	485 490 495	
	TCC CCC CCA GCT GAC CAG ACC CTG GTC ATC AAG ACA TTC CGC TTC CTG	1536
	Ser Pro Pro Ala Asp Gln Thr Leu Val Ile Lys Thr Phe Arg Phe Leu	
20	500 505 510	
	TCA CAG AAA CTC TTT ATC TCC GTC TCA GTT CTC TCC AGC CTG GGC ATT	1584
	Ser Gln Lys Leu Phe Ile Ser Val Ser Val Leu Ser Ser Leu Gly Ile	
	515 520 525	
25	GTC CTA GCT GTT GTC TGT CTG TCC TTT AAC ATC TAC AAC TCA CAT GTC	1632
	Val Leu Ala Val Val Cys Leu Ser Phe Asn Ile Tyr Asn Ser His Val	
	530 535 540	
30	CGT TAT ATC CAG AAC TCA CAG CCC AAC CTG AAC AAC CTG ACT GCT GTG	1680
	Arg Tyr Ile Gln Asn Ser Gln Pro Asn Leu Asn Asn Leu Thr Ala Val	
	545 550 555 560	
	GGC TGC TCA CTG GCT TTA GCT GCT GTC TTC CCC CTG GGG CTC GAT GGT	1728
35	Gly Cys Ser Leu Ala Leu Ala Ala Val Phe Pro Leu Gly Leu Asp Gly	
	565 570 575	
	TAC CAC ATT GGG AGG AAC CAG TTT CCT TTC GTC TGC CAG GCC CGC CTC	1776
	Tyr His Ile Gly Arg Asn Gln Phe Pro Phe Val Cys Gln Ala Arg Leu	
40	580 585 590	
	TGG CTC CTG GGC CTG GGC TTT AGT CTG GGC TAC GGT TCC ATG TTC ACC	1824
	Trp Leu Leu Gly Leu Gly Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr	

	595	600	605	
	AAG ATT TGG TGG GTC CAC ACG GTC TTC ACA AAG AAG GAA GAA AAG AAG			1872
	Lys Ile Trp Trp Val His Thr Val Phe Thr Lys Lys Glu Glu Lys Lys			
5	610	615	620	
	GAG TGG AGG AAG ACT CTG GAA CCC TGG AAG CTG TAT GCC ACA GTG GGC			1920
	Glu Trp Arg Lys Thr Leu Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly			
	625	630	635	640
10				
	CTG CTG GTG GGC ATG GAT GTC CTC ACT CTC GCC ATC TGG CAG ATC GTG			1968
	Leu Leu Val Gly Met Asp Val Leu Thr Leu Ala Ile Trp Gln Ile Val			
	645	650	655	
15	GAC CCT CTG CAC CGG ACC ATT GAG ACA TTT GCC AAG GAG GAA CCT AAG			2016
	Asp Pro Leu His Arg Thr Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys			
	660	665	670	
	GAA GAT ATT GAC GTC TCT ATT CTG CCC CAG CTG GAG CAT TGC AGC TCC			2064
20	Glu Asp Ile Asp Val Ser Ile Leu Pro Gln Leu Glu His Cys Ser Ser			
	675	680	685	
	AGG AAG ATG AAT ACA TGG CTT GGC ATT TTC TAT GGT TAC AAG GGG CTG			2112
	Arg Lys Met Asn Thr Trp Leu Gly Ile Phe Tyr Gly Tyr Lys Gly Leu			
25	690	695	700	
	CTG CTG CTG CTG GGA ATC TTC CTT GCT TAT GAG ACC AAG AGT GTG TCC			2160
	Leu Leu Leu Leu Gly Ile Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser			
	705	710	715	720
30				
	ACT GAG AAG ATC AAT GAT CAC CGG GCT GTG GGC ATG GCT ATC TAC AAT			2208
	Thr Glu Lys Ile Asn Asp His Arg Ala Val Gly Met Ala Ile Tyr Asn			
	725	730	735	
35	GTG GCA GTC CTG TGC CTC ATC ACT GCT CCT GTC ACC ATG ATT CTG TCC			2256
	Val Ala Val Leu Cys Leu Ile Thr Ala Pro Val Thr Met Ile Leu Ser			
	740	745	750	
	AGC CAG CAG GAT GCA GCC TTT GCC TTT GCC TCT CTT GCC ATA GTT TTC			2304
40	Ser Gln Gln Asp Ala Ala Phe Ala Phe Ala Ser Leu Ala Ile Val Phe			
	755	760	765	
	TCC TCC TAT ATC ACT CTT GTT GTG CTC TTT GTG CCC AAG ATG CGC AGG			2352

	Ser	Ser	Tyr	Ile	Thr	Leu	Val	Val	Leu	Phe	Val	Pro	Lys	Met	Arg	Arg	
	770						775					780					
	CTG	ATC	ACC	CGA	GGG	GAA	TGG	CAG	TCG	GAG	GCG	CAG	GAC	ACC	ATG	AAG	2400
5	Leu	Ile	Thr	Arg	Gly	Glu	Trp	Gln	Ser	Glu	Ala	Gln	Asp	Thr	Met	Lys	
	785					790					795					800	
	ACA	GGG	TCA	TCG	ACC	AAC	AAC	AAC	GAG	GAG	GAG	AAG	TCC	CGG	CTG	TTG	2448
	Thr	Gly	Ser	Ser	Thr	Asn	Asn	Asn	Glu	Glu	Glu	Lys	Ser	Arg	Leu	Leu	
10					805					810					815		
	GAG	AAG	GAG	AAC	CGT	GAA	CTG	GAA	AAG	ATC	ATT	GCT	GAG	AAA	GAG	GAG	2496
	Glu	Lys	Glu	Asn	Arg	Glu	Leu	Glu	Lys	Ile	Ile	Ala	Glu	Lys	Glu	Glu	
				820					825					830			
15	CGT	GTC	TCT	GAA	CTG	CGC	CAT	CAA	CTC	CAG	TCT	CGG	CAG	CAG	CTC	CGC	2544
	Arg	Val	Ser	Glu	Leu	Arg	His	Gln	Leu	Gln	Ser	Arg	Gln	Gln	Leu	Arg	
		835					840					845					
20	TCC	CGG	CGC	CAC	CCA	CCG	ACA	CCC	CCA	GAA	CCC	TCT	GGG	GGC	CTG	CCC	2592
	Ser	Arg	Arg	His	Pro	Pro	Thr	Pro	Pro	Glu	Pro	Ser	Gly	Gly	Leu	Pro	
		850					855					860					
	AGG	GGA	CCC	CCT	GAG	CCC	CCC	GAC	CGG	CTT	AGC	TGT	GAT	GGG	AGT	CGA	2640
25	Arg	Gly	Pro	Pro	Glu	Pro	Pro	Asp	Arg	Leu	Ser	Cys	Asp	Gly	Ser	Arg	
	865					870					875				880		
	GTG	CAT	TTG	CTT	TAT	AAG	TGA										2661
	Val	His	Leu	Leu	Tyr	Lys	*										
30						885											

(2) INFORMATION FOR SEQ ID NO: 77:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 886 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:



Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly  
 1 5 10 15  
 Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile  
 5 20 25 30  
 Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg  
 35 40 45  
 10 Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu  
 50 55 60  
 Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys  
 65 70 75 80  
 15 Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys  
 85 90 95  
 Val Asn Arg Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly Ala  
 20 100 105 110  
 Leu Phe Pro Ala Val Glu Met Ala Leu Glu Asp Val Asn Ser Arg Arg  
 115 120 125  
 25 Asp Ile Leu Pro Asp Tyr Glu Leu Lys Leu Ile His His Asp Ser Lys  
 130 135 140  
 Cys Asp Pro Gly Gln Ala Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn  
 145 150 155 160  
 30 Asp Pro Ile Lys Ile Ile Leu Met Pro Gly Cys Ser Ser Val Ser Thr  
 165 170 175  
 Leu Val Ala Glu Ala Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr  
 35 180 185 190  
 Gly Ser Ser Ser Pro Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe  
 195 200 205  
 40 Phe Arg Thr His Pro Ser Ala Thr Leu His Asn Pro Thr Arg Val Lys  
 210 215 220  
 Leu Phe Glu Lys Trp Gly Trp Lys Lys Ile Ala Thr Ile Gln Gln Thr

	225		230			235			240								
	Thr	Glu	Val	Phe	Thr	Ser	Thr	Leu	Asp	Asp	Leu	Glu	Glu	Arg	Val	Lys	
					245					250					255		
5	Glu	Ala	Gly	Ile	Glu	Ile	Thr	Phe	Arg	Gln	Ser	Phe	Phe	Ser	Asp	Pro	
					260					265					270		
	Ala	Val	Pro	Val	Lys	Asn	Leu	Lys	Arg	Gln	Asp	Ala	Arg	Ile	Ile	Val	
10					275					280					285		
	Gly	Leu	Phe	Tyr	Glu	Thr	Glu	Ala	Arg	Lys	Val	Phe	Cys	Glu	Val	Tyr	
					290					295					300		
15	Lys	Glu	Arg	Leu	Phe	Gly	Lys	Lys	Tyr	Val	Trp	Phe	Leu	Ile	Gly	Trp	
					305					310					315		320
	Tyr	Ala	Asp	Asn	Trp	Phe	Lys	Ile	Tyr	Asp	Pro	Ser	Ile	Asn	Cys	Thr	
					325					330					335		
20	Val	Asp	Glu	Met	Thr	Glu	Ala	Val	Glu	Gly	His	Ile	Thr	Thr	Glu	Ile	
					340					345					350		
	Val	Met	Leu	Asn	Pro	Ala	Asn	Thr	Arg	Ser	Ile	Ser	Asn	Met	Thr	Ser	
25					355					360					365		
	Gln	Glu	Phe	Val	Glu	Lys	Leu	Thr	Lys	Arg	Leu	Lys	Arg	His	Pro	Glu	
					370					375					380		
30	Glu	Thr	Gly	Gly	Phe	Gln	Glu	Ala	Pro	Leu	Ala	Tyr	Asp	Ala	Ile	Trp	
					385					390					395		400
	Ala	Leu	Ala	Leu	Ala	Leu	Asn	Lys	Thr	Ser	Gly	Gly	Gly	Gly	Arg	Ser	
					405					410					415		
35	Gly	Val	Arg	Leu	Glu	Asp	Phe	Asn	Tyr	Asn	Asn	Gln	Thr	Ile	Thr	Asp	
					420					425					430		
	Gln	Ile	Tyr	Arg	Ala	Met	Asn	Ser	Ser	Ser	Phe	Glu	Gly	Val	Ser	Gly	
40					435					440					445		
	His	Val	Val	Phe	Asp	Ala	Ser	Gly	Ser	Arg	Met	Ala	Trp	Thr	Leu	Ile	
					450					455					460		

Glu Gln Leu Gln Gly Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser  
 465 470 475 480

5 Thr Lys Asp Asp Leu Ser Trp Ser Lys Thr Asp Lys Trp Ile Gly Gly  
 485 490 495

Ser Pro Pro Ala Asp Gln Thr Leu Val Ile Lys Thr Phe Arg Phe Leu  
 500 505 510

10 Ser Gln Lys Leu Phe Ile Ser Val Ser Val Leu Ser Ser Leu Gly Ile  
 515 520 525

Val Leu Ala Val Val Cys Leu Ser Phe Asn Ile Tyr Asn Ser His Val  
 15 530 535 540

Arg Tyr Ile Gln Asn Ser Gln Pro Asn Leu Asn Asn Leu Thr Ala Val  
 545 550 555 560

20 Gly Cys Ser Leu Ala Leu Ala Ala Val Phe Pro Leu Gly Leu Asp Gly  
 565 570 575

Tyr His Ile Gly Arg Asn Gln Phe Pro Phe Val Cys Gln Ala Arg Leu  
 580 585 590

25 Trp Leu Leu Gly Leu Gly Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr  
 595 600 605

Lys Ile Trp Trp Val His Thr Val Phe Thr Lys Lys Glu Glu Lys Lys  
 30 610 615 620

Glu Trp Arg Lys Thr Leu Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly  
 625 630 635 640

35 Leu Leu Val Gly Met Asp Val Leu Thr Leu Ala Ile Trp Gln Ile Val  
 645 650 655

Asp Pro Leu His Arg Thr Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys  
 660 665 670

40 Glu Asp Ile Asp Val Ser Ile Leu Pro Gln Leu Glu His Cys Ser Ser  
 675 680 685

Arg Lys Met Asn Thr Trp Leu Gly Ile Phe Tyr Gly Tyr Lys Gly Leu  
 690 695 700

Leu Leu Leu Leu Gly Ile Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser  
 5 705 710 715 720

Thr Glu Lys Ile Asn Asp His Arg Ala Val Gly Met Ala Ile Tyr Asn  
 725 730 735

10 Val Ala Val Leu Cys Leu Ile Thr Ala Pro Val Thr Met Ile Leu Ser  
 740 745 750

Ser Gln Gln Asp Ala Ala Phe Ala Phe Ala Ser Leu Ala Ile Val Phe  
 755 760 765

15 Ser Ser Tyr Ile Thr Leu Val Val Leu Phe Val Pro Lys Met Arg Arg  
 770 775 780

Leu Ile Thr Arg Gly Glu Trp Gln Ser Glu Ala Gln Asp Thr Met Lys  
 20 785 790 795 800

Thr Gly Ser Ser Thr Asn Asn Asn Glu Glu Glu Lys Ser Arg Leu Leu  
 805 810 815

25 Glu Lys Glu Asn Arg Glu Leu Glu Lys Ile Ile Ala Glu Lys Glu Glu  
 820 825 830

Arg Val Ser Glu Leu Arg His Gln Leu Gln Ser Arg Gln Gln Leu Arg  
 835 840 845

30 Ser Arg Arg His Pro Pro Thr Pro Pro Glu Pro Ser Gly Gly Leu Pro  
 850 855 860

Arg Gly Pro Pro Glu Pro Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg  
 35 865 870 875 880

Val His Leu Leu Tyr Lys  
 885

40

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1692 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

10

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

15

(B) LOCATION:1..1692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

20	ATG TTG CTG CTG CTG CTA CTG GCG CCA CTC TTC CTC CGC CCC CCG GGC	48
	Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly	
	1 5 10 15	
25	GCG GGC GGG GCG CAG ACC CCC AAC GCC ACC TCA GAA GGT TGC CAG ATC	96
	Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile	
	20 25 30	
30	ATA CAC CCG CCC TGG GAA GGG GGC ATC AGG TAC CGG GGC CTG ACT CGG	144
	Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg	
	35 40 45	
35	GAC CAG GTG AAG GCT ATC AAC TTC CTG CCA GTG GAC TAT GAG ATT GAG	192
	Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu	
	50 55 60	
35	TAT GTG TGC CGG GGG GAG CGC GAG GTG GTG GGG CCC AAG GTC CGC AAG	240
	Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys	
	65 70 75 80	
40	TGC CTG GCC AAC GGC TCC TGG ACA GAT ATG GAC ACA CCC AGC CGC TGT	288
	Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys	
	85 90 95	
	GTC CGA ATC TGC TCC AAG TCT TAT TTG ACC ATT ACC GAC CAA ATC TAC	336

	Val	Arg	Ile	Cys	Ser	Lys	Ser	Tyr	Leu	Thr	Ile	Thr	Asp	Gln	Ile	Tyr	
				100					105					110			
	CGG	GCA	ATG	AAC	TCT	TCG	TCC	TTT	GAG	GGT	GTC	TCT	GGC	CAT	GTG	GTG	384
5	Arg	Ala	Met	Asn	Ser	Ser	Ser	Phe	Glu	Gly	Val	Ser	Gly	His	Val	Val	
			115					120					125				
	TTT	GAT	GCC	AGC	GGC	TCT	CGG	ATG	GCA	TGG	ACG	CTT	ATC	GAG	CAG	CTT	432
	Phe	Asp	Ala	Ser	Gly	Ser	Arg	Met	Ala	Trp	Thr	Leu	Ile	Glu	Gln	Leu	
10		130					135					140					
	CAG	GGT	GGC	AGC	TAC	AAG	AAG	ATT	GGC	TAC	TAT	GAC	AGC	ACC	AAG	GAT	480
	Gln	Gly	Gly	Ser	Tyr	Lys	Lys	Ile	Gly	Tyr	Tyr	Asp	Ser	Thr	Lys	Asp	
	145					150					155				160		
15																	
	GAT	CTT	TCC	TGG	TCC	AAA	ACA	GAT	AAA	TGG	ATT	GGA	GGG	TCC	CCC	CCA	528
	Asp	Leu	Ser	Trp	Ser	Lys	Thr	Asp	Lys	Trp	Ile	Gly	Gly	Ser	Pro	Pro	
					165					170				175			
20	GCT	GAC	CAG	ACC	CTG	GTC	ATC	AAG	ACA	TTC	CGC	TTC	CTG	TCA	CAG	AAA	576
	Ala	Asp	Gln	Thr	Leu	Val	Ile	Lys	Thr	Phe	Arg	Phe	Leu	Ser	Gln	Lys	
				180					185					190			
	CTC	TTT	ATC	TCC	GTC	TCA	GTT	CTC	TCC	AGC	CTG	GGC	ATT	GTC	CTA	GCT	624
25	Leu	Phe	Ile	Ser	Val	Ser	Val	Leu	Ser	Ser	Leu	Gly	Ile	Val	Leu	Ala	
			195					200					205				
	GTT	GTC	TGT	CTG	TCC	TTT	AAC	ATC	TAC	AAC	TCA	CAT	GTC	CGT	TAT	ATC	672
	Val	Val	Cys	Leu	Ser	Phe	Asn	Ile	Tyr	Asn	Ser	His	Val	Arg	Tyr	Ile	
30		210					215					220					
	CAG	AAC	TCA	CAG	CCC	AAC	CTG	AAC	AAC	CTG	ACT	GCT	GTG	GGC	TGC	TCA	720
	Gln	Asn	Ser	Gln	Pro	Asn	Leu	Asn	Asn	Leu	Thr	Ala	Val	Gly	Cys	Ser	
	225					230					235				240		
35																	
	CTG	GCT	TTA	GCT	GCT	GTC	TTC	CCC	CTG	GGG	CTC	GAT	GGT	TAC	CAC	ATT	768
	Leu	Ala	Leu	Ala	Ala	Val	Phe	Pro	Leu	Gly	Leu	Asp	Gly	Tyr	His	Ile	
				245					250					255			
40	GGG	AGG	AAC	CAG	TTT	CCT	TTC	GTC	TGC	CAG	GCC	CGC	CTC	TGG	CTC	CTG	816
	Gly	Arg	Asn	Gln	Phe	Pro	Phe	Val	Cys	Gln	Ala	Arg	Leu	Trp	Leu	Leu	
				260					265					270			

	GGC CTG GGC TTT AGT CTG GGC TAC GGT TCC ATG TTC ACC AAG ATT TGG	854
	Gly Leu Gly Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr Lys Ile Trp	
	275 280 285	
5	TGG GTC CAC ACG GTC TTC ACA AAG AAG GAA GAA AAG AAG GAG TGG AGG	912
	Trp Val His Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp Arg	
	290 295 300	
	AAG ACT CTG GAA CCC TGG AAG CTG TAT GCC ACA GTG GGC CTG CTG GTG	960
10	Lys Thr Leu Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly Leu Leu Val	
	305 310 315 320	
	GGC ATG GAT GTC CTC ACT CTC GCC ATC TGG CAG ATC GTG GAC CCT CTG	1008
15	Gly Met Asp Val Leu Thr Leu Ala Ile Trp Gln Ile Val Asp Pro Leu	
	325 330 335	
	CAC CGG ACC ATT GAG ACA TTT GCC AAG GAG GAA CCT AAG GAA GAT ATT	1056
	His Arg Thr Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys Glu Asp Ile	
	340 345 350	
20	GAC GTC TCT ATT CTG CCC CAG CTG GAG CAT TGC AGC TCC AGG AAG ATG	1104
	Asp Val Ser Ile Leu Pro Gln Leu Glu His Cys Ser Ser Arg Lys Met	
	355 360 365	
25	AAT ACA TGG CTT GGC ATT TTC TAT GGT TAC AAG GGG CTG CTG CTG CTG	1152
	Asn Thr Trp Leu Gly Ile Phe Tyr Gly Tyr Lys Gly Leu Leu Leu Leu	
	370 375 380	
	CTG GGA ATC TTC CTT GCT TAT GAG ACC AAG AGT GTG TCC ACT GAG AAG	1200
30	Leu Gly Ile Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser Thr Glu Lys	
	385 390 395 400	
	ATC AAT GAT CAC CGG GCT GTG GGC ATG GCT ATC TAC AAT GTG GCA GTC	1248
35	Ile Asn Asp His Arg Ala Val Gly Met Ala Ile Tyr Asn Val Ala Val	
	405 410 415	
	CTG TGC CTC ATC ACT GCT CCT GTC ACC ATG ATT CTG TCC AGC CAG CAG	1296
	Leu Cys Leu Ile Thr Ala Pro Val Thr Met Ile Leu Ser Ser Gln Gln	
	420 425 430	
40	GAT GCA GCC TTT GCC TTT GCC TCT CTT GCC ATA GTT TTC TCC TCC TAT	1344
	Asp Ala Ala Phe Ala Phe Ala Ser Leu Ala Ile Val Phe Ser Ser Tyr	
	435 440 445	

ATC ACT CTT GTT GTG CTC TTT GTG CCC AAG ATG CGC AGG CTG ATC ACC 1392  
 Ile Thr Leu Val Val Leu Phe Val Pro Lys Met Arg Arg Leu Ile Thr  
 450 455 460

5 CGA GGG GAA TGG CAG TCG GAG GCG CAG GAC ACC ATG AAG ACA GGG TCA 1440  
 Arg Gly Glu Trp Gln Ser Glu Ala Gln Asp Thr Met Lys Thr Gly Ser  
 465 470 475 480

10 TCG ACC AAC AAC AAC GAG GAG GAG AAG TCC CGG CTG TTG GAG AAG GAG 1488  
 Ser Thr Asn Asn Asn Glu Glu Glu Lys Ser Arg Leu Leu Glu Lys Glu  
 485 490 495

AAC CGT GAA CTG GAA AAG ATC ATT GCT GAG AAA GAG GAG CGT GTC TCT 1536  
 15 Asn Arg Glu Leu Glu Lys Ile Ile Ala Glu Lys Glu Glu Arg Val Ser  
 500 505 510

GAA CTG CGC CAT CAA CTC CAG TCT CGG CAG CAG CTC CGC TCC CGG CGC 1584  
 Glu Leu Arg His Gln Leu Gln Ser Arg Gln Gln Leu Arg Ser Arg Arg  
 20 515 520 525

CAC CCA CCG ACA CCC CCA GAA CCC TCT GGG GGC CTG CCC AGG GGA CCC 1632  
 His Pro Pro Thr Pro Pro Glu Pro Ser Gly Gly Leu Pro Arg Gly Pro  
 530 535 540

25 CCT GAG CCC CCC GAC CGG CTT AGC TGT GAT GGG AGT CGA GTG CAT TTG 1680  
 Pro Glu Pro Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg Val His Leu  
 545 550 555 560

30 CTT TAT AAG TGA 1692  
 Leu Tyr Lys \*

35 (2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 563 amino acids

(B) TYPE: amino acid

40 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly  
 1 5 10 15  
 5 Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile  
 20 25 30  
 10 Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg  
 35 40 45  
 Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu  
 50 55 60  
 15 Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys  
 65 70 75 80  
 Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys  
 85 90 95  
 20 Val Arg Ile Cys Ser Lys Ser Tyr Leu Thr Ile Thr Asp Gln Ile Tyr  
 100 105 110  
 Arg Ala Met Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val Val  
 25 115 120 125  
 Phe Asp Ala Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln Leu  
 130 135 140  
 30 Gln Gly Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys Asp  
 145 150 155 160  
 Asp Leu Ser Trp Ser Lys Thr Asp Lys Trp Ile Gly Gly Ser Pro Pro  
 165 170 175  
 35 Ala Asp Gln Thr Leu Val Ile Lys Thr Phe Arg Phe Leu Ser Gln Lys  
 180 185 190  
 Leu Phe Ile Ser Val Ser Val Leu Ser Ser Leu Gly Ile Val Leu Ala  
 40 195 200 205  
 Val Val Cys Leu Ser Phe Asn Ile Tyr Asn Ser His Val Arg Tyr Ile  
 210 215 220

Gln Asn Ser Gln Pro Asn Leu Asn Asn Leu Thr Ala Val Gly Cys Ser  
 225 230 235 240

5 Leu Ala Leu Ala Ala Val Phe Pro Leu Gly Leu Asp Gly Tyr His Ile  
 245 250 255

Gly Arg Asn Gln Phe Pro Phe Val Cys Gln Ala Arg Leu Trp Leu Leu  
 260 265 270

10 Gly Leu Gly Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr Lys Ile Trp  
 275 280 285

Trp Val His Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp Arg  
 15 290 295 300

Lys Thr Leu Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly Leu Leu Val  
 305 310 315 320

20 Gly Met Asp Val Leu Thr Leu Ala Ile Trp Gln Ile Val Asp Pro Leu  
 325 330 335

His Arg Thr Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys Glu Asp Ile  
 340 345 350

25 Asp Val Ser Ile Leu Pro Gln Leu Glu His Cys Ser Ser Arg Lys Met  
 355 360 365

Asn Thr Trp Leu Gly Ile Phe Tyr Gly Tyr Lys Gly Leu Leu Leu Leu  
 30 370 375 380

Leu Gly Ile Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser Thr Glu Lys  
 385 390 395 400

35 Ile Asn Asp His Arg Ala Val Gly Met Ala Ile Tyr Asn Val Ala Val  
 405 410 415

Leu Cys Leu Ile Thr Ala Pro Val Thr Met Ile Leu Ser Ser Gln Gln  
 420 425 430

40 Asp Ala Ala Phe Ala Phe Ala Ser Leu Ala Ile Val Phe Ser Ser Tyr  
 435 440 445

Ile Thr Leu Val Val Leu Phe Val Pro Lys Met Arg Arg Leu Ile Thr  
 450 455 460

Arg Gly Glu Trp Gln Ser Glu Ala Gln Asp Thr Met Lys Thr Gly Ser  
 5 465 470 475 480

Ser Thr Asn Asn Asn Glu Glu Glu Lys Ser Arg Leu Leu Glu Lys Glu  
 485 490 495

10 Asn Arg Glu Leu Glu Lys Ile Ile Ala Glu Lys Glu Glu Arg Val Ser  
 500 505 510

Glu Leu Arg His Gln Leu Gln Ser Arg Gln Gln Leu Arg Ser Arg Arg  
 515 520 525

15 His Pro Pro Thr Pro Pro Glu Pro Ser Gly Gly Leu Pro Arg Gly Pro  
 530 535 540

Pro Glu Pro Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg Val His Leu  
 20 545 550 555 560

Leu Tyr Lys

25

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2602 base pairs  
 30 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

35

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

40

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION:1..318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

	ATG TTG CTG CTG CTG CTA CTG GCG CCA CTC TTC CTC CGC CCC CCG GGC	48
5	Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly	
	1 5 10 15	
	GCG GGC GGG GCG CAG ACC CCC AAC GCC ACC TCA GAA GGT TGC CAG ATC	96
	Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile	
10	20 25 30	
	ATA CAC CCG CCC TGG GAA GGG GGC ATC AGG TAC CGG GGC CTG ACT CGG	144
	Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg	
	35 40 45	
15	GAC CAG GTG AAG GCT ATC AAC TTC CTG CCA GTG GAC TAT GAG ATT GAT	192
	Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Asp	
	50 55 60	
20	GAA TCG AAC GCC ACA CTC AGA ACG GCG CGC AGT GTA CAT CGG GGC ACT	240
	Glu Ser Asn Ala Thr Leu Arg Thr Ala Arg Ser Val His Arg Gly Thr	
	65 70 75 80	
	GTT TCC CAT GAG CGG GGG CTG GCC AGG GGG CCA GGC CTG CCA GCC CGC	288
25	Val Ser His Glu Arg Gly Leu Ala Arg Gly Pro Gly Leu Pro Ala Arg	
	85 90 95	
	GGT GGA GAT GGC GCT GGA GGA CGT GAA TAG CCGCAGGGAC ATCCTGCCGG	338
	Gly Gly Asp Gly Ala Gly Gly Arg Glu *	
30	100 105	
	ACTATGAGCT CAAGCTCATC CACCACGACA GCAAGTGTGA TCCAGGCCAA GCCACCAAGT	398
	ACCTATATGA GCTGCTCTAC AACGACCCTA TCAAGATCAT CCTTATGCCT GGCTGCAGCT	458
35	CTGTCTCCAC GCTGGTGGCT GAGGCTGCTA GGATGTGGAA CCTCATTTGTG CTTTCCTATG	518
	GCTCCAGCTC ACCAGCCCTG TCAAACCGGC AGCGTTTCCC CACTTTCTTC CGAACGCACC	578
40	CATCAGCCAC ACTCCACAAC CCTACCCGCG TGAAACTCTT TGAAAAGTGG GGCTGGAAGA	638
	AGATTGCTAC CATCCAGCAG ACCACTGAGG TCTTCACTTC GACTCTGGAC GACCTGGAGG	698

	AACGAGTGAA GGAGGCTGGA ATTGAGATTA CTTTCCGCCA GAGTTTCTTC TCAGATCCAG	758
	CTGTGCCCCGT CAAAAACCTG AAGCGCCAGG ATGCCCGAAT CATCGTGGGA CTTTCTATG	818
5	AGACTGAAGC CCGGAAAGTT TTTTGTGAGG TGTACAAGGA GCGTCTCTTT GGGAAGAAGT	878
	ACGTCTGGTT CCTCATTGGG TGGTATGCTG ACAATTGGTT CAAGATCTAC GACCCTTCTA	938
	TCAACTGCAC AGTGGATGAG ATGACTGAGG CGGTGGAGGG CCACATCACA ACTGAGATTG	998
10	TCATGCTGAA TCCTGCCAAT ACCCGCAGCA TTTCCAACAT GACATCCCAG GAATTTGTGG	1058
	AGAAACTAAC CAAGCGACTG AAAAGACACC CTGAGGAGAC AGGAGGCTTC CAGGAGGCAC	1118
15	CGCTGGCCTA TGATGCCATC TGGGCCTTGG CACTGGCCCT GAACAAGACA TCTGGAGGAG	1178
	GCGGCCGTTC TGGTGTGCGC CTGGAGGACT TCAACTACAA CAACCAGACC ATTACCGACC	1238
	AAATCTACCG GGCAATGAAC TCTTCGTCCT TTGAGGGTGT CTCTGGCCAT GTGGTGTTTG	1298
20	ATGCCAGCGG CTCTCGGATG GCATGGACGC TTATCGAGCA GCTTCAGGGT GGCAGCTACA	1358
	AGAAGATTGG CTA CTATGAC AGCACCAAGG ATGATCTTTC CTGGTCCAAA ACAGATAAAT	1418
25	GGATTGGAGG GTCCCCCCA GCTGACCAGA CCCTGGTCAT CAAGACATTC CGCTTCCTGT	1478
	CACAGAAACT CTTTATCTCC GTCTCAGTTC TCTCCAGCCT GGGCATTGTC CTAGCTGTTG	1538
	TCTGTCTGTC CTTTAACATC TACAACTCAC ATGTCCGTTA TATCCAGAAC TCACAGCCCA	1598
30	ACCTGAACAA CCTGACTGCT GTGGGCTGCT CACTGGCTTT AGCTGCTGTC TTCCCCCTGG	1658
	GGCTCGATGG TTACCACATT GGGAGGAACC AGTTTCCTTT CGTCTGCCAG GCCCGCCTCT	1718
35	GGCTCCTGGG CCTGGGCTTT AGTCTGGGCT ACGGTTCCAT GTTCACCAAG ATTTGGTGGG	1778
	TCCACACGGT CTTACAAAG AAGGAAGAAA AGAAGGAGTG GAGGAAGACT CTGGAACCCT	1838
	GGAAGCTGTA TGCCACAGTG GGCCTGCTGG TGGGCATGGA TGTCTCACT CTCGCCATCT	1898
40	GGCAGATCGT GGACCCTCTG CACCGGACCA TTGAGACATT TGCCAAGGAG GAACCTAAGG	1958
	AAGATATTGA CGTCTCTATT CTGCCCCAGC TGGAGCATTG CAGCTCCAGG AAGATGAATA	2018

CATGGCTTGG CATTCTCTAT GGTTACAAGG GGCTGCTGCT GCTGCTGGGA ATCTTCCTTG 2078  
 CTTATGAGAC CAAGAGTGTG TCCACTGAGA AGATCAATGA TCACCGGGCT GTGGGCATGG 2138  
 5 CTATCTACAA TGTGGCAGTC CTGTGCCTCA TCACTGCTCC TGTCACCATG ATTCTGTCCA 2198  
 GCCAGCAGGA TGCAGCCTTT GCCTTTGCCT CTCTTGCCAT AGTTTTCTCC TCCTATATCA 2258  
 10 CTCTTGTTGT GCTCTTTGTG CCCAAGATGC GCAGGCTGAT CACCCGAGGG GAATGGCAGT 2318  
 CGGAGGCGCA GGACACCATG AAGACAGGGT CATCGACCAA CAACAACGAG GAGGAGAAGT 2378  
 CCCGGCTGTT GGAGAAGGAG AACCGTGAAC TGGAAAAGAT CATTGCTGAG AAAGAGGAGC 2438  
 15 GTGTCTCTGA ACTGCGCCAT CAACTCCAGT CTCGGCAGCA GCTCCGCTCC CGGCGCCACC 2498  
 CACCGACACC CCCAGAACCC TCTGGGGGCC TGCCCAGGGG ACCCCCTGAG CCCCCGACC 2558  
 20 GGCTTAGCTG TGATGGGAGT CGAGTGCATT TGCTTTATAA GTGA 2602

## (2) INFORMATION FOR SEQ ID NO: 81:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

Met Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly  
 35 1 5 10 15  
 Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile  
 20 25 30  
 40 Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg  
 35 40 45  
 Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Asp

	50		55		60	
	Glu Ser Asn Ala Thr	Leu Arg Thr Ala Arg Ser Val His Arg Gly Thr				
	65	70	75	80		
5	Val Ser His Glu Arg Gly Leu Ala Arg Gly Pro Gly Leu Pro Ala Arg					
	85	90	95			
	Gly Gly Asp Gly Ala Gly Gly Arg Glu					
10	100	105				

(2) INFORMATION FOR SEQ ID NO: 82:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2367 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## 20

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

25 (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

30 (B) LOCATION:1..294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

	ATG	TTG	CTG	CTG	CTG	CTA	CTG	GCG	CCA	CTC	TTC	CTC	GCG	CCC	CCG	GGC	48
35	Met	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Pro	Leu	Phe	Leu	Arg	Pro	Pro	Gly	
	1				5					10					15		
	GCG	GGC	GGG	GCG	CAG	ACC	CCC	AAC	GCC	ACC	TCA	GAA	GGT	TGC	CAG	ATC	96
	Ala	Gly	Gly	Ala	Gln	Thr	Pro	Asn	Ala	Thr	Ser	Glu	Gly	Cys	Gln	Ile	
40				20					25					30			
	ATA	CAC	CCG	CCC	TGG	GAA	GGG	GGC	ATC	AGG	TAC	CGG	GGC	CTG	ACT	CGG	144
	Ile	His	Pro	Pro	Trp	Glu	Gly	Gly	Ile	Arg	Tyr	Arg	Gly	Leu	Thr	Arg	

	35	40	45	
	GAC CAG GTG AAG GCT ATC AAC TTC CTG CCA GTG GAC TAT GAG ATT GAG	192		
	Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu			
5	50	55	60	
	TAT GTG TGC CGG GGG GAG CGC GAG GTG GTG GGG CCC AAG GTC CGC AAG	240		
	Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys			
	65	70	75	80
10				
	TGC CTG GCC AAC GGC TCC TGG ACA GAT ATG GAC ACA CCC AGC CGC TGT	288		
	Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys			
	85	90	95	
15	GTG TGA TCCAGGCCAA GCCACCAAGT ACCTATATGA GCTGCTCTAC AACGACCCTA	344		
	Val *			
	TCAAGATCAT CCTTATGCCT GGCTGCAGCT CTGTCTCCAC GCTGGTGGCT GAGGCTGCTA	404		
20				
	GGATGTGGAA CCTCATTTGTG CTTTCCTATG GCTCCAGCTC ACCAGCCCTG TCAAACCGGC	464		
	AGCGTTTCCC CACTTTCTTC CGAACGCACC CATCAGCCAC ACTCCACAAC CCTACCCGCG	524		
25	TGAAACTCTT TGAAAAGTGG GGCTGGAAGA AGATTGCTAC CATCCAGCAG ACCACTGAGG	584		
	TCTTCACTTC GACTCTGGAC GACCTGGAGG AACGAGTGAA GGAGGCTGGA ATTGAGATTA	644		
	CTTTCGCCCA GAGTTTCTTC TCAGATCCAG CTGTGCCCCGT CAAAACCTG AAGCGCCAGG	704		
30				
	ATGCCCCGAAT CATCGTGGGA CTTTCTATG AGACTGAAGC CCGGAAAGTT TTTTGTGAGG	764		
	TGTACAAGGA GCGTCTCTTT GGGAAGAAGT ACGTCTGGTT CCTCATTTGGG TGGTATGCTG	824		
35	ACAATTGGTT CAAGATCTAC GACCCTTCTA TCAACTGCAC AGTGGATGAG ATGACTGAGG	884		
	CGGTGGAGGG CCACATCACA ACTGAGATTG TCATGCTGAA TCCTGCCAAT ACCCGCAGCA	944		
	TTTCCAACAT GACATCCCAG GAATTTGTGG AGAACTAAC CAAGCGACTG AAAAGACACC	1004		
40				
	CTGAGGAGAC AGGAGGCTTC CAGGAGGCAC CGCTGGCCTA TGATGCCATC TGGGCCTTGG	1064		
	CACTGGCCCT GAACAAGACA TCTGGAGGAG GCGGCCGTTC TGGTGTGCGC CTGGAGGACT	1124		



	TCAACTACAA CAACCAGACC ATTACCGACC AAATCTACCG GGCAATGAAC TCTTCGTCCT	1184
	TTGAGGGTGT CTCTGGCCAT GTGGTGTGTTG ATGCCAGCGG CTCTCGGATG GCATGGACGC	1244
5	TTATCGAGCA GCTTCAGGGT GGCAGCTACA AGAAGATTGG CTACTATGAC AGCACCAAGG	1304
	ATGATCTTTC CTGGTCCAAA ACAGATAAAT GGATTGTTAT ATCCAGAACT CACAGCCCAA	1364
10	CCTGAACAAC CTGACTGCTG TGGGCTGCTC ACTGGCTTTA GCTGCTGTCT TCCCCCTGGG	1424
	GCTCGATGGT TACCACATTG GGAGGAACCA GTTTCCTTTC GTCTGCCAGG CCCGCCTCTG	1484
	GCTCCTGGGC CTGGGCTTTA GTCTGGGCTA CGGTTCCATG TTCACCAAGA TTTGGTGGGT	1544
15	CCACACGGTC TTCACAAAGA AGGAAGAAAA GAAGGAGTGG AGGAAGACTC TGGAACCCTG	1604
	GAAGCTGTAT GCCACAGTGG GCCTGCTGGT GGGCATGGAT GTCCTCACTC TCGCCATCTG	1664
20	GCAGATCGTG GACCCTCTGC ACCGGACCAT TGAGACATTT GCCAAGGAGG AACCTAAGGA	1724
	AGATATTGAC GTCTCTATTC TGCCCCAGCT GGAGCATTGC AGCTCCAGGA AGATGAATAC	1784
	ATGGCTTGGC ATTTTCTATG GTTACAAGGG GCTGCTGCTG CTGCTGGGAA TCTTCCTTGC	1844
25	TTATGAGACC AAGAGTGTGT CCACTGAGAA GATCAATGAT CACCGGGCTG TGGGCATGGC	1904
	TATCTACAAT GTGGCAGTCC TGTGCCTCAT CACTGCTCCT GTCACCATGA TTCTGTCCAG	1964
30	CCAGCAGGAT GCAGCCTTTG CCTTTGCCTC TCTTGCCATA GTTTTCTCCT CCTATATCAC	2024
	TCTTGTTGTG CTCTTTGTGC CCAAGATGCG CAGGCTGATC ACCCGAGGGG AATGGCAGTC	2084
	GGAGGCGCAG GACACCATGA AGACAGGGTC ATCGACCAAC AACAACGAGG AGGAGAAGTC	2144
35	CCGGCTGTTG GAGAAGGAGA ACCGTGAACT GGAAAAGATC ATTGCTGAGA AAGAGGAGCG	2204
	TGTCTCTGAA CTGCGCCATC AACTCCAGTC TCGGCAGCAG CTCCGCTCCC GGCGCCACCC	2264
40	ACCGACACCC CCAGAACCCT CTGGGGGCCT GCCCAGGGGA CCCCCTGAGC CCCCCGACCG	2324
	GCTTAGCTGT GATGGGAGTC GAGTGCATTT GCTTTATAAG TGA	2367

## (2) INFORMATION FOR SEQ ID NO: 83:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 97 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly  
 1 5 10 15  
 15 Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile  
 20 25 30  
 Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg  
 20 35 40 45  
 Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu  
 50 55 60  
 25 Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys  
 65 70 75 80  
 Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys  
 85 90 95  
 30 Val

## 35 (2) INFORMATION FOR SEQ ID NO: 84:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 2489 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

10

(A) NAME/KEY: CDS

(B) LOCATION:1..1491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

15	ATG TTG CTG CTG CTG CTA CTG GCG CCA CTC TTC CTC CGC CCC CCG GGC	48
	Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly	
	1                      5                      10                      15	
	GCG GGC GGG GCG CAG ACC CCC AAC GCC ACC TCA GAA GGT TGC CAG ATC	96
20	Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile	
	20                      25                      30	
	ATA CAC CCG CCC TGG GAA GGG GGC ATC AGG TAC CGG GGC CTG ACT CGG	144
	Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg	
25	35                      40                      45	
	GAC CAG GTG AAG GCT ATC AAC TTC CTG CCA GTG GAC TAT GAG ATT GAG	192
	Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu	
	50                      55                      60	
30	TAT GTG TGC CGG GGG GAG CGC GAG GTG GTG GGG CCC AAG GTC CGC AAG	240
	Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys	
	65                      70                      75                      80	
35	TGC CTG GCC AAC GGC TCC TGG ACA GAT ATG GAC ACA CCC AGC CGC TGT	288
	Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys	
	85                      90                      95	
	GTC CGA ATC TGC TCC AAG TCT TAT TTG ACC CTG GAA AAT GGG AAG GTT	336
40	Val Arg Ile Cys Ser Lys Ser Tyr Leu Thr Leu Glu Asn Gly Lys Val	
	100                      105                      110	
	TTC CTG ACG GGT GGG GAC CTC CCA GCT CTG GAC GGA GCC CGG GTG GAT	384

	Phe	Leu	Thr	Gly	Gly	Asp	Leu	Pro	Ala	Leu	Asp	Gly	Ala	Arg	Val	Asp		
	115						120						125					
	TTC	CGG	TGT	GAC	CCC	GAC	TTC	CAT	CTG	TGT	GAT	CCA	GGC	CAA	GCC	ACC	432	
5	Phe	Arg	Cys	Asp	Pro	Asp	Phe	His	Leu	Cys	Asp	Pro	Gly	Gln	Ala	Thr		
	130						135						140					
	AAG	TAC	CTA	TAT	GAG	CTG	CTC	TAC	AAC	GAC	CCT	ATC	AAG	ATC	ATC	CTT	480	
	Lys	Tyr	Leu	Tyr	Glu	Leu	Leu	Tyr	Asn	Asp	Pro	Ile	Lys	Ile	Ile	Leu		
10	145						150						155			160		
	ATG	CCT	GGC	TGC	AGC	TCT	GTC	TCC	ACG	CTG	GTG	GCT	GAG	GCT	GCT	AGG	528	
	Met	Pro	Gly	Cys	Ser	Ser	Val	Ser	Thr	Leu	Val	Ala	Glu	Ala	Ala	Arg		
				165						170						175		
15	ATG	TGG	AAC	CTC	ATT	GTG	CTT	TCC	TAT	GGC	TCC	AGC	TCA	CCA	GCC	CTG	576	
	Met	Trp	Asn	Leu	Ile	Val	Leu	Ser	Tyr	Gly	Ser	Ser	Ser	Pro	Ala	Leu		
	180						185						190					
20	TCA	AAC	CGG	CAG	CGT	TTC	CCC	ACT	TTC	TTC	CGA	ACG	CAC	CCA	TCA	GCC	624	
	Ser	Asn	Arg	Gln	Arg	Phe	Pro	Thr	Phe	Phe	Arg	Thr	His	Pro	Ser	Ala		
	195						200						205					
	ACA	CTC	CAC	AAC	CCT	ACC	CGC	GTG	AAA	CTC	TTT	GAA	AAG	TGG	GGC	TGG	672	
25	Thr	Leu	His	Asn	Pro	Thr	Arg	Val	Lys	Leu	Phe	Glu	Lys	Trp	Gly	Trp		
	210						215						220					
	AAG	AAG	ATT	GCT	ACC	ATC	CAG	CAG	ACC	ACT	GAG	GTC	TTC	ACT	TCG	ACT	720	
	Lys	Lys	Ile	Ala	Thr	Ile	Gln	Gln	Thr	Thr	Glu	Val	Phe	Thr	Ser	Thr		
30	225						230						235			240		
	CTG	GAC	GAC	CTG	GAG	GAA	CGA	GTG	AAG	GAG	GCT	GGA	ATT	GAG	ATT	ACT	768	
	Leu	Asp	Asp	Leu	Glu	Glu	Arg	Val	Lys	Glu	Ala	Gly	Ile	Glu	Ile	Thr		
				245						250						255		
35	TTC	CGC	CAG	AGT	TTC	TTC	TCA	GAT	CCA	GCT	GTG	CCC	GTC	AAA	AAC	CTG	816	
	Phe	Arg	Gln	Ser	Phe	Phe	Ser	Asp	Pro	Ala	Val	Pro	Val	Lys	Asn	Leu		
	260						265						270					
40	AAG	CGC	CAG	GAT	GCC	CGA	ATC	ATC	GTG	GGA	CTT	TTC	TAT	GAG	ACT	GAA	864	
	Lys	Arg	Gln	Asp	Ala	Arg	Ile	Ile	Val	Gly	Leu	Phe	Tyr	Glu	Thr	Glu		
	275						280						285					

	GCC CGG AAA GTT TTT TGT GAG GTG TAC AAG GAG CGT CTC TTT GGG AAG	912
	Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly Lys	
	290 295 300	
5	AAG TAC GTC TGG TTC CTC ATT GGG TGG TAT GCT GAC AAT TGG TTC AAG	960
	Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe Lys	
	305 310 315 320	
	ATC TAC GAC CCT TCT ATC AAC TGC ACA GTG GAT GAG ATG ACT GAG GCG	1008
10	Ile Tyr Asp Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr Glu Ala	
	325 330 335	
	GTG GAG GGC CAC ATC ACA ACT GAG ATT GTC ATG CTG AAT CCT GCC AAT	1056
	Val Glu Gly His Ile Thr Thr Glu Ile Val Met Leu Asn Pro Ala Asn	
15	340 345 350	
	ACC CGC AGC ATT TCC AAC ATG ACA TCC CAG GAA TTT GTG GAG AAA CTA	1104
	Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu Lys Leu	
	355 360 365	
20	ACC AAG CGA CTG AAA AGA CAC CCT GAG GAG ACA GGA GGC TTC CAG GAG	1152
	Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln Glu	
	370 375 380	
25	GCA CCG CTG GCC TAT GAT GCC ATC TGG GCC TTG GCA CTG GCC CTG AAC	1200
	Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Leu Asn	
	385 390 395 400	
	AAG ACA TCT GGA GGA GGC GGC CGT TCT GGT GTG CGC CTG GAG GAC TTC	1248
30	Lys Thr Ser Gly Gly Gly Arg Ser Gly Val Arg Leu Glu Asp Phe	
	405 410 415	
	AAC TAC AAC AAC CAG ACC ATT ACC GAC CAA ATC TAC CGG GCA ATG AAC	1296
	Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala Met Asn	
35	420 425 430	
	TCT TCG TCC TTT GAG GGT GTC TCT GGC CAT GTG GTG TTT GAT GCC AGC	1344
	Ser Ser Ser Phe Glu Gly Val Ser Gly His Val Val Phe Asp Ala Ser	
	435 440 445	
40	GGC TCT CGG ATG GCA TGG ACG CTT ATC GAG CAG CTT CAG GGT GGC AGC	1392
	Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly Gly Ser	
	450 455 460	

	TAC AAG AAG ATT GGC TAC TAT GAC AGC ACC AAG GAT GAT CTT TCC TGG	1440
	Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu Ser Trp	
	465 470 475 480	
5	TCC AAA ACA GAT AAA TGG ATT GTT ATA TCC AGA ACT CAC AGC CCA ACC	1488
	Ser Lys Thr Asp Lys Trp Ile Val Ile Ser Arg Thr His Ser Pro Thr	
	485 490 495	
10	TGA ACAACCTGAC TGCTGTGGGC TGCTCACTGG CTTTAGCTGC TGTCTTCCCC	1541
	*	
	CTGGGGCTCG ATGGTTACCA CATTGGGAGG AACCAGTTTC CTTTCGTCTG CCAGGCCCGC	1601
15	CTCTGGCTCC TGGGCCTGGG CTTTAGTCTG GGCTACGGTT CCATGTTTAC CAAGATTGG	1661
	TGGGTCCACA CGGTCTTAC AAAGAAGGAA GAAAAGAAG AGTGGAGGAA GACTCTGGAA	1721
20	CCCTGGAAGC TGTATGCCAC AGTGGGCCTG CTGGTGGGCA TGGATGTCCT CACTCTCGCC	1781
	ATCTGGCAGA TCGTGGACCC TCTGCACCGG ACCATTGAGA CATTTGCCAA GGAGGAACCT	1841
	AAGGAAGATA TTGACGTCTC TATTCTGCCC CAGCTGGAGC ATTGCAGCTC CAGGAAGATG	1901
25	AATACATGGC TTGGCATTTC CTATGGTTAC AAGGGGCTGC TGCTGCTGCT GGGAACTCTC	1961
	CTTGCTTATG AGACCAAGAG TGTGTCCACT GAGAAGATCA ATGATCACCG GGCTGTGGGC	2021
30	ATGGCTATCT ACAATGTGGC AGTCCTGTGC CTCATCACTG CTCCTGTCAC CATGATTCTG	2081
	TCCAGCCAGC AGGATGCAGC CTTTGCCTTT GCCTCTCTTG CCATAGTTTT CTCCTCCTAT	2141
	ATCACTCTTG TTGTGCTCTT TGTGCCCAAG ATGCGCAGGC TGATCACCCG AGGGGAATGG	2201
35	CAGTCGGAGG CGCAGGACAC CATGAAGACA GGGTCATCGA CCAACAACAA CGAGGAGGAG	2261
	AAGTCCCGGC TGTGGAGAA GGAGAACCGT GAACTGGAAA AGATCATTGC TGAGAAAGAG	2321
40	GAGCGTGTCT CTGAAGTGGC CCATCAACTC CAGTCTCGGC AGCAGCTCCG CTCCCGGCGC	2381
	CACCCACCGA CACCCCCAGA ACCCTCTGGG GGCTGCCCCA GGGGACCCCC TGAGCCCCC	2441

GACCGGCTTA GCTGTGATGG GAGTCGAGTG CATTTGCTTT ATAAGTGA

2489

## (2) INFORMATION FOR SEQ ID NO: 85:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 496 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

15 Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly  
 1 5 10 15

Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile  
 20 25 30

20

Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg  
 35 40 45

25 Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu  
 50 55 60

Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys  
 65 70 75 80

30 Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys  
 85 90 95

Val Arg Ile Cys Ser Lys Ser Tyr Leu Thr Leu Glu Asn Gly Lys Val  
 100 105 110

35

Phe Leu Thr Gly Gly Asp Leu Pro Ala Leu Asp Gly Ala Arg Val Asp  
 115 120 125

40 Phe Arg Cys Asp Pro Asp Phe His Leu Cys Asp Pro Gly Gln Ala Thr  
 130 135 140

Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile Ile Leu  
 145 150 155 160

Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala Arg  
165 170 175

5 Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala Leu  
180 185 190

Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro Ser Ala  
195 200 205

10 Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp Gly Trp  
210 215 220

Lys Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr Ser Thr  
15 225 230 235 240

Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu Ile Thr  
245 250 255

20 Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys Asn Leu  
260 265 270

Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu Thr Glu  
275 280 285

25 Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly Lys  
290 295 300

Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe Lys  
30 305 310 315 320

Ile Tyr Asp Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr Glu Ala  
325 330 335

35 Val Glu Gly His Ile Thr Thr Glu Ile Val Met Leu Asn Pro Ala Asn  
340 345 350

Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu Lys Leu  
355 360 365

40 Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln Glu  
370 375 380



Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Asn  
385 390 395 400

Lys Thr Ser Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu Asp Phe  
5 405 410 415

Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala Met Asn  
420 425 430

10 Ser Ser Ser Phe Glu Gly Val Ser Gly His Val Val Phe Asp Ala Ser  
435 440 445

Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly Gly Ser  
450 455 460

15 Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu Ser Trp  
465 470 475 480

Ser Lys Thr Asp Lys Trp Ile Val Ile Ser Arg Thr His Ser Pro Thr  
20 485 490 495



## INTERNATIONAL SEARCH REPORT

International application No.

PCT/SE 98/01947

<b>A. CLASSIFICATION OF SUBJECT MATTER</b>		
<b>IPC6: C07K 14/705</b> According to International Patent Classification (IPC) or to both national classification and IPC		
<b>B. FIELDS SEARCHED</b>		
Minimum documentation searched (classification system followed by classification symbols)		
IPC6: C07K		
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched		
SE,DK,FI,NO classes as above		
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)		
<b>C. DOCUMENTS CONSIDERED TO BE RELEVANT</b>		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	EMBL Databas Genbank/DBJ, accession no. Y11044, Grifa A. et al: "GABA (gamma-amino-butyric acid)neurotransmission: identification and fine mapping of human GABA-B receptor gene"; Biochem. Biophys. Res. Commun. 250:240-245(1998) --	1-6,11-13, 16-26
X	Nature, Volume 386, March 1997, Klemens Kaupmann et al, "Expression cloning of GABAB receptors uncovers similarity to metabotropic glutamate receptors" page 239 - page 246 --	1-6,11-13, 16-26
X	WO 9746675 A1 (NOVARTIS AG), 11 December 1997 (11.12.97), page 50 - page 56, claim 4 --	1-6,11-13, 16-26
<input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C. <input checked="" type="checkbox"/> See patent family annex.		
* Special categories of cited documents: "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier document but published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance: the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance: the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art "&" document member of the same patent family		
Date of the actual completion of the international search		Date of mailing of the international search report
23 March 1999		26-03- 1999
Name and mailing address of the ISA Swedish Patent Office Box 5055, S-102 42 STOCKHOLM Facsimile No. +46 8 666 02 86		Authorized officer Patrick Andersson Telephone No. +46 8 782 25 00

# INTERNATIONAL SEARCH REPORT

International application No.

PCT/SE 98/01947

## C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	<p>Dialog Information Services, File 34,  SciSearch, Dialog accession no. 07157158,  Goei VL et al: "Human gamma-aminobutyric  acid B receptor gene: Complementary DNA  cloning, expression, chromosomal location,  and genomic organization", Biological  Psychiatry, 1998, V44, N8(OCT 15), p659-666</p> <p>--</p>	<p>1-6,11-13,  16-26</p>
A	<p>Brain Research Bulletin, Volume 38, No 6, 1995,  Robert J. Washabau et al, "GABA Receptros in the  Dorsal Motor Nucleus of the Vagus Influence Feline  Lower Esophageal Sphincter and Gastric Function"  page 587 - page 594</p> <p>--  -----</p>	<p>1-6,11-13,  16-26</p>

# INTERNATIONAL SEARCH REPORT

International application No. \_\_\_\_\_

PCT/SE 98/01947

## Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
  
2. ☐ Claims Nos.:  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
  
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

See next page

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
  
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐

The additional search fees were accompanied by the applicant's protest.

☐

No protest accompanied the payment of additional search fees.

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/SE 98/01947

According to PCT rule 13.2, an international application shall relate to one invention only or a group of inventions linked by one or more of the same or corresponding "special technical features", i.e. features that define a contribution which each of the inventions makes over the prior art.

The claimed invention relates to a nucleic acid sequence encoding a GABAB-receptor from either human or canine origin. A possible special technical features could have been nucleotide sequence encoding a GABAB-receptor. However a nucleotide sequence encoding a human GABAB-receptor is known from Grifa A. et. al., see the search report. Thus, the present application is considered to contain the following independent inventions:

Invention 1, claims 3-4, and the parts of claims 1-2 and 16-26 relating to claims 3-4: A human GABAB-receptor 1a, and related items,

Invention 2, claims 5-6, and the parts of claims 1-2 and 16-26 relating to claims 5-6: A human GABAB-receptor 1b, and related items,

Invention 3, claims 7-8, and the parts of claims 1-2 and 16-26 relating to claims 7-8: A human GABAB-receptor 1c, and related items,

Invention 4, claims 9-10, and the parts of claims 1-2 and 16-26 relating to claims 9-10: A human GABAB-receptor 1d, and related items,

Invention 5, claims 12-13, and the parts of claims 1, 11 and 16-26 relating to claims 12-13: A canine GABAB-receptor 1a, and related items.

Invention 6, claims 14-15, and the parts of claims 1, 11 and 16-26 relating to claims 14-15: A canine GABAB-receptor 1c, and related items.

The search has been limited to inventions 1, 2 and 5.

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Form PCT/ISA:210 (patent family annex) (July 1992)